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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 14:17:52 ; Search time 3116 Seconds
(without alignments)
5884.072 Million cell updates/sec

Title: US-09-820-339A-1
Perfect score: 630
Sequence: 1 tccgaacatgagaccgctct.....acttcgtcatgcagcgccgtg 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
tal number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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41:	em_htgo_other.*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	630	100.0	630	6	A83283	A83283 Sequence 3
2	628.4	99.7	1599	9	BC006314	BC006314 Homo sapi
3	628.4	99.7	1667	9	HSACHRA	Y00762 Human mRNA
4	628.4	99.7	1676	9	S77094	S77094 nicotinic a
5	623.6	99.0	645	12	SYNHUMACRS	M64695 Synthetic h
6	564.4	89.6	3618	4	BTACHRAL	X02509 B.Taurus mr
7	561.2	89.1	1380	4	AB021708	AB021708 Canis fam
8	526	83.5	1769	10	MUSACHRAM	X03986 Mouse mRNA
9	526	83.5	1860	10	MUSACHRAM	M17640 Mus musculu
10	522.8	83.0	1849	10	RNACHRA1	X74832 R.norvegicu
11	426.8	67.7	1393	5	GA250359	AJ250359 Gallus ga
12	354	56.2	2045	5	FSCACHRA	J00963 Ray (T.calli
13	350.8	55.7	1350	6	AR106255	AR106255 Sequence
14	350.8	55.7	1815	5	FSCACHR	M25893 T.marmorata
15	348	55.2	1421	5	XLACHRA	X07067 Xenopus mrn
16	345.8	54.9	1408	5	XLACHRA1	X17244 Xenopus mrn
17	316.4	50.2	2218	5	DRU70438	U70438 Danio rerio
18	228.4	36.3	1956	4	BTACHRECA	X57032 B.taurus mr
19	226.4	35.9	1756	6	AR055253	AR055253 Sequence
20	226.4	35.9	1756	6	AR071401	AR071401 Sequence
21	226.4	35.9	1756	6	AR173185	AR173185 Sequence
22	225.2	35.7	1425	9	HSNACHRA3	X53559 H.sapiens H
23	225.2	35.7	1471	9	AF385584	AF385584 Homo sapi
24	225.2	35.7	2046	9	BC006114	BC006114 Homo sapi
25	224.2	35.6	1590	9	HSY16281	Y16281 Homo sapien
26	224.2	35.6	2277	6	AR037435	AR037435 Sequence
27	224.2	35.6	2664	9	HSU62431	U62431 Human nicot
28	223.6	35.5	1512	9	HSNACHRA3A	Y08418 H.sapiens m
29	223.6	35.5	1908	9	HSU62432	U62432 Human nicot
30	223.6	35.5	1910	9	HUMNNAR	M37981 Human alpha
31	223.6	35.5	3020	9	BC002996	BC002996 Homo sapi
32	223.6	35.5	3029	9	BC000513	BC000513 Homo sapi
33	223.6	35.5	3029	9	BC001642	BC001642 Homo sapi
34	222.6	35.3	1608	5	GA250360	AJ250360 Gallus ga
35	222	35.2	1858	10	RATNARA	L31621 Rattus norv
36	222	35.2	1932	10	RNACHRAR	X03440 Rat mrna fo
37	221.6	35.2	252	4	EEU17016	U17016 Erinaceus c
38	221.6	35.1	3540	10	BC011490	BC011490 Mus muscu
39	220.4	35.0	1058	10	AF325346	AF325346 Mus muscu
40	220.4	35.0	1612	10	AF472588	AF472588 Mus muscu
41	220.4	35.0	1783	10	AF459029	AF459029 Mus muscu
42	219.4	34.8	1954	10	AF225912	AF225912 Mus muscu
43	217.8	34.6	1884	9	HSNACHRA4	Y08421 H.sapiens m
44	217.8	34.6	3343	9	HSU62433	U62433 Human nicot
45	217.2	34.5	1584	9	HUMA3NARSP	M86383 Homo sapien

ALIGNMENTS

RESULT 1

A83283	A83283	Sequence 3 from Patent WO9850544.	630 bp	DNA	linear	PAT 21-JAN-2000
LOCUS	DEFINITION	Sequence 3 from Patent WO9850544.				
ACCESSION	VERSION	A83283.1	GI:6732701			
KEYWORDS	SOURCE	human.				
ORGANISM	ORGANISM	Homo sapiens				
REFERENCE	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	TITLE	1 (bases 1 to 630)				
		Barchan,D. and Fuchs,S.				
		RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND THEIR				
		USE FOR TREATMENT OF MYASTHENIA GRAVIS				

JOURNAL Patent: WO 9850544-A 3 12-NOV-1998;
BARCHAN DORA (IL); FUCHS SARA (IL)
FEATURES Location/Qualifiers
source 1..630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="EXTRACELLULAR DOMAIN OF ACETYLCHOLINE RECEPTOR ALPHA-SUBUNIT"
BASE COUNT 165 a 174 c 159 g 132 t
ORIGIN
Query Match 100.0%; Score 630; DB 6; Length 630;
Best Local Similarity 100.0%; Pred. No. 1.5e-136;
Matches 630; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCCGAACATGAGACCCGCTGCTGTCGCAAGCTATTAAAGACTACAGCAGCGTGTGCGG 60
Db 1 TCCGAACATGAGACCCGCTGCTGTCGCAAGCTATTAAAGACTACAGCAGCGTGTGCGG 60
61 CCAGTGGAGACCCAGCGCTGAGGTCACCGTGGGCTGCAGCTGATACAGCTC 120
61 CCAGTGGAGACCCAGCGCTGAGGTCACCGTGGGCTGCAGCTGATACAGCTC 120
QY 121 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGCGCTGAAACAGCAATGG 180
Db 121 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGCGCTGAAACAGCAATGG 180
QY 181 GTGGATTACAACTAAATGGAATCCAGATGACTATGCGGTGTGAAAAAATTCACATT 240
Db 181 GTGGATTACAACTAAATGGAATCCAGATGACTATGCGGTGTGAAAAAATTCACATT 240
QY 241 CTTTCAGAAAGATCTGGGCCAGACCTTGTCTCTATAGGATGCGAGTGGTACATTT 300
Db 241 CTTTCAGAAAGATCTGGGCCAGACCTTGTCTCTATAGGATGCGAGTGGTACATTT 300
QY 301 GCTATTGTCAAGTTCACCAAGTCTGCTGCAGTACACTGCGCATACATGCGACCT 360
Db 301 GCTATTGTCAAGTTCACCAAGTCTGCTGCAGTACACTGCGCATACATGCGACCT 360
QY 361 CCAGCCATCTTTAAAGCTACTGTGAGATCATGCTGACCCACTTTCCCTTTGATGAACAG 420
Db 361 CCAGCCATCTTTAAAGCTACTGTGAGATCATGCTGACCCACTTTCCCTTTGATGAACAG 420
QY 421 AACTGCAGATGAAGCTGGGACCTGGACCTAGCAGGCTCTGTGCTGGGCAATCAACCG 480
Db 421 AACTGCAGATGAAGCTGGGACCTGGACCTAGCAGGCTCTGTGCTGGGCAATCAACCG 480
QY 481 GAAAGCAGCAGCAGCAGCTGAGCAACTTCATGGAGCGGGAGTGGTATCAAGGAG 540
Db 481 GAAAGCAGCAGCAGCAGCTGAGCAACTTCATGGAGCGGGAGTGGTATCAAGGAG 540
QY 541 TCCCGGGCTGGAAGCACTCCGCTGACCTATTCTCTGCTGCCCGACACCCCTTACCTGGAC 600
Db 541 TCCCGGGCTGGAAGCACTCCGCTGACCTATTCTCTGCTGCCCGACACCCCTTACCTGGAC 600
QY 601 ATCACTACCACTTGGTATGATGAGCGGCTG 630
Db 601 ATCACTACCACTTGGTATGATGAGCGGCTG 630

RESULT 2
LOCUS BC006314 1599 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, Similar to cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle), clone MGC:12708 IMAGE:4124038, mRNA, complete cds.
ACCESSION BC006314
VERSION BC006314.1 GI:13623428
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1599)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgrl.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 17 Row: g Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557456.
FEATURES
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1..1599
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/db_xref="taxon:9606"
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/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
69..878
/codon_start=1
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/protein_id="AAH06314.1"
/db_xref="GI:13623429"
/translation="MEPRLILLFLSCAGLVGSEHETRLVAKLFDKDYSSVRPVED HRQVETVGLQLIQLINVDENVQITTVNLKQKQWVDYLNKWPDDYGGVKRIHPS EKIMRDLVLYNNADGFAIVKFTKLLQYTHITWTPPAIFKSYCYIIVHFFPDEQ NCSMKLTWTYDGSVAIVNSDQDPLSNFMESEWYIKESRGKHSVTVSCCPDTPY LDITYHFVMQRLPLYFIVNVIIPLCLFSLTGLVFLYPLTDSGGCGCHDCC"
BASE COUNT 425 a 432 c 365 g 377 t
ORIGIN
Query Match 99.7%; Score 628.4; DB 9; Length 1599;
Best Local Similarity 99.8%; Pred. No. 3.9e-136;
Matches 629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCGAACATGAGACCCGCTGCTGTCGCAAGCTATTAAAGACTACAGCAGCGTGTGCGG 60
Db 129 TCCGAACATGAGACCCGCTGCTGTCGCAAGCTATTAAAGACTACAGCAGCGTGTGCGG 188
QY 61 CCAGTGGAGACCCAGCGCTGAGGTCACCGTGGGCTGCAGCTGATACAGCTC 120
Db 189 CCAGTGGAGACCCAGCGCTGAGGTCACCGTGGGCTGCAGCTGATACAGCTC 248
QY 121 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGCGCTGAAACAGCAATGG 180
Db 249 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGCGCTGAAACAGCAATGG 308
QY 181 GTGGATTACAACTAAATGGAATCCAGATGACTATGCGGTGTGAAAAAATTCACATT 240
Db 309 GTGGATTACAACTAAATGGAATCCAGATGACTATGCGGTGTGAAAAAATTCACATT 368

QY 241 CCTTCAAGAAAGATCTGGCCAGACCTTGTCTCTATACGATGAGATGGTACTTT 300
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Db 369 CCTTCAAGAAAGATCTGGCCAGACCTTGTCTCTATACGATGAGATGGTACTTT 428
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QY 301 GCTATTGCAAGTTCACCAAGTGTCTCTGAGTACACTGGCCACATCAGTGGACACCT 360
Db 429 GCTATTGCAAGTTCACCAAGTGTCTCTGAGTACACTGGCCACATCAGTGGACACCT 488
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QY 361 CCAGCCATCTTTAAAGCTACTGTGAGATCATGCTACCCACCTTCCCTTTGATGAACAG 420
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Db 489 CCAGCCATCTTTAAAGCTACTGTGAGATCATGCTACCCACCTTCCCTTTGATGAACAG 548
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QY 421 AACTGCAAGTTCACCAAGTGTCTCTGAGTACACTGGCCACATCAGTGGACACCT 480
Db 549 AACTGCAAGTTCACCAAGTGTCTCTGAGTACACTGGCCACATCAGTGGACACCT 608
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QY 481 GAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540
Db 609 GAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 668
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QY 541 TCCCGGGCTGGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600
Db 569 TCCCGGGCTGGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 728
|||||

RESULT 3

HSACHRA
LOCUS
DEFINITION Human mRNA for muscle acetylcholine receptor alpha subunit.
VERSION Y00762
ACCESSION Y00762.1 GI:28308
KEYWORDS acetylcholine receptor alpha.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1667)
Schoepfer, R.
Direct Submission
JOURNAL Submitted (03-FEB-1988)
REFERENCE 2 (bases 1 to 1667)
Schoepfer, R., Luther, M. and Lindstrom, J.
TITLE The human medulloblastoma cell line TE671 expresses a muscle-like
acetylcholine receptor. Cloning of the alpha-subunit cDNA
FEBS Lett. 226 (2), 235-240 (1988)
88112190
3338555

.FEATURES

Location/Qualifiers

1..1667

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="pTE1.1"

/cell_line="medulloblastoma TE761"

/clone_lib="ITE"

49..1422

/note="precursor (AA -20 to 437)"

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/protein_id="CAA68731.1"

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/translation="MEPWLLLLSLCSAGLVGSEHETRLVAKLFKDYSSVVRPVED
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NCSMKLGYDGSVVAINPESQDPLSNFMSGEWIKESRGWKSHTYSCPDTPY
LDITVHFVWRPLPLFIVNIIPLCLFSLTGLVFLPTDSEKMTLSISLILTVF
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CDS

source

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sig_peptide

mat_peptide

misc_feature

BASE COUNT 419 a 465 c 371 g 412 t

ORIGIN

Query Match 99.7%; Score 628.4; DB 9; Length 1667;

Best Local Similarity 99.8%; Pred. No. 3.9e-136;

Matches 629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGAACATGAGACCCCTCTGTGGCAAAAGCTATTTAAAGACTACACGAGCGTGGTGGG 60

Db 109 TCCGAACATGAGACCCCTCTGTGGCAAAAGCTATTTAAAGACTACACGAGCGTGGTGGG 168

QY 61 CCAGTGAAGACACACCCCGAGTGTGGAGTCACTGGGCTGCGAGTATACAGCTC 120

Db 169 CCAGTGAAGACACACCCCGAGTGTGGAGTCACTGGGCTGCGAGTATACAGCTC 228

QY 121 ATCAATGTGATGAAGTAAATCAGATCGTGACACCAATGTGGCTCTGAAACACGCAATGG 180

Db 229 ATCAATGTGATGAAGTAAATCAGATCGTGACACCAATGTGGCTCTGAAACACGCAATGG 288

QY 181 GTGATTACAACTTAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTCACATT 240

Db 289 GTGATTACAACTTAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTCACATT 348

QY 241 CTTTCAGAAAGATCTGGGCGCCAGACCTTGTCTCTATAAGTGCAGATGGTACTTT 300

Db 349 CTTTCAGAAAGATCTGGGCGCCAGACCTTGTCTCTATAAGTGCAGATGGTACTTT 408

QY 301 GCTATTGCAAGTTCACCAAGTGTCTCTGAGTACACTGGCCACATCAGTGGACACCT 360

Db 409 GCTATTGCAAGTTCACCAAGTGTCTCTGAGTACACTGGCCACATCAGTGGACACCT 468

QY 361 CCAGCCATCTTTAAAGCTACTGTGAGATCATCTGCCACTTCCCTTTGATGAACAG 420

Db 469 CCAGCCATCTTTAAAGCTACTGTGAGATCATCTGCCACTTCCCTTTGATGAACAG 528

QY 421 AACTGCAAGTGAAGTGGGACCTGGACCTGACACGGCTCTGTCGGGCGCATCAACCG 480

Db 529 AACTGCAAGTGAAGTGGGACCTGGACCTGACACGGCTCTGTCGGGCGCATCAACCG 588

QY 481 GAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 540

Db 589 GAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 648

QY 541 TCCCGGGCTGGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 600

Db 649 TCCCGGGCTGGGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 708

QY 501 ATCACTTACCACTTCGTGATGACGCGCTG 630

Db 709 ATCACTTACCACTTCGTGATGACGCGCTG 738

RESULT 4

S77094

LOCUS

DEFINITION

S77094

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

S77094 1676 bp mRNA linear PRI 26-SEP-1995
nicotinic acetylcholine receptor alpha subunit [AChR alpha subunit
human, thymic carcinoma, myasthenia gravis-associated thymoma
patient 1494/88, mRNA Partial, 1676 nt].

S77094.1 GI:998469

Homo sapiens thymic carcinoma myasthenia gravis-associated thymoma

patient 1494/88.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1676)

AUTHORS Gattenlohner S., Brabletz T., Schultz A., Marx A.,
Muller-Hermelink H.K. and Kirchner T.
TITLE Cloning of a cDNA coding for the acetylcholine receptor
alpha-subunit from a thymoma associated with myasthenia [correction
of myasthenia] gravis
JOURNAL Thymus 23 (2), 103-113 (1994)
MEDLINE 95242389
PUBMED 7725386
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gibbsq 164456] from the original journal article.

FEATURES
Location/Qualifiers
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KSALEGKIYATNWKSDQESNNAAREKYNVAMWMDHLLGVFLVCLIGLAVFAGRL
IELNQGG"

BASE COUNT 428 a 463 c 370 g 415 t
ORIGIN
Query Match 99.7%; Score 628.4; DB 9; Length 1676;
Best Local Similarity 99.8%; Pred. No. 3.9e-136;
Matches 629; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCGAACATGAGACCCGCTCTGGTGCAAGCTATTATAAGACTACAGCAGCGTGGTGGCG 60
DB 109 TCCGAACATGAGACCCGCTCTGGTGCAAGCTATTATAAGACTACAGCAGCGTGGTGGCG 168
QY 61 CCAGTGGGAAGACCCGCGAGGTGTGAGGTCCAGCTCCGCTGGCGCTGCAGCTGATACAGCTC 120
DB 169 CCAGTGGGAAGACCCGCGAGGTGTGAGGTCCAGCTCCGCTGGCGCTGCAGCTGATACAGCTC 228
QY 121 ATCAATGTGGATGAAGTAAATCAGATCTGACACCAATGTGCGTCTGAAACAGCAATGG 180
DB 229 ATCAATGTGGATGAAGTAAATCAGATCTGACACCAATGTGCGTCTGAAACAGCAATGG 288
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DB 289 GTGGATTACAACTAAATGGAATCCAGATGACTATGCGGTGTGAAACCAATTCACATT 348
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DB 349 CCTTCAGAAAAGATCTGGCGCCAGACCTTGTCTCTATAACATGACAGATGGTGACTTT 408
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DB 409 GCTATTGTCAAGTTCCACAAAGTGTCTCTGAGTACACTGGCGCTACACCTGACAGTCCCT 468
QY 361 CCAGCCATCTTTAAAGTACTGTGAGATCATCGTACCCACTTTCCTTTTATGAAACAG 420
DB 469 CCAGCCATCTTTAAAGTACTGTGAGATCATCGTACCCACTTTCCTTTTATGAAACAG 528
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DB 529 AACTCCAGATGAGCTGGGACCTGGACCTACGACGCTCTGCTGGCCATCAACCCG 588
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DB 589 GAAACGACAGCCAGACCTGAGCAACTTCATGGAGAGGGGGAGTGGGTGATCAAGGAG 648
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DB 649 TCCCGGGCTGGAAGCACTCCGTGACCTATTCTCTGCTCCCGACACACCCCTACCTGGAC 708
QY 601 ATCACTACCACTTCGTGTCATGACGCGCTG 630
DB 709 ATCACTACCACTTCGTGTCATGACGCGCTG 738
RESULT 5
SYNHUMACRS SYNTHUMACRS 645 bp DNA linear SYN 27-APR-1993
LOCUS SYNTHUMACRS 645 bp DNA linear SYN 27-APR-1993
DEFINITION Synthetic human acetylcholine receptor alpha subunit gene, complete cds.
ACCESSION M64695
VERSION M64695.1 GI:208505
KEYWORDS acetylcholine receptor subunit-alpha.
SOURCE Synthetic DNA.
ORGANISM artificial construct
artificial sequences.
REFERENCE 1 (bases 1 to 645)
AUTHORS Talib,S., Leiby,K.R., Wright,K. and Okarma,T.B.
TITLE Cloning and expression in Escherichia coli of a synthetic gene encoding the extracellular domain of the human muscle acetylcholine receptor alpha-subunit
JOURNAL Gene 98 (2), 289-293 (1991)
MEDLINE 91200680
PUBMED 2016069
FEATURES Location/Qualifiers
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/db_xref="GI:208506"
/translation="MSEHETRLVAKLFKDYSSVVRPVEDHRQVEYTVGLQLQLINVDENVQIVTNVRLKQWDYNLKNPDDYGGVKRIHIPSERKINRPDLVLYNADGDFAIKFTKVLQYTHITWTPPAIFKSYCEIIVTHFFPDEQNCESMKLGTWYDGSVVAIPESDQPLSNFMESEGEWIKESRGWKHSVTYSCCPDTPYLDITVHFVQLRL"
BASE COUNT 172 a 177 c 158 g 138 t
ORIGIN
Query Match 99.0%; Score 623.6; DB 12; Length 645;
Best Local Similarity 99.4%; Pred. No. 4.8e-135;
Matches 626; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 TCCGAACATGAGACCCGCTCTGGTGCAAGCTATTATAAGACTACAGCAGCGTGGTGGCG 60
DB 9 TCCGAACATGAGACCCGCTCTGGTGCAAGCTATTATAAGACTACAGCAGCGTGGTGGCG 68
QY 61 CCAGTGGGAAGACCCGCGAGGTGTGAGGTCCAGCTCCGCTGGCGCTGATACAGCTC 120
DB 69 CCAGTGGGAAGACCCGCGAGGTGTGAGGTCCAGCTCCGCTGGCGCTGATACAGCTC 128
QY 121 ATCAATGTGGATGAAGTAAATCAGATCTGACACCAATGTGCGGTGTGAAACCAATTCACATT 180
DB 129 ATCAATGTGGATGAAGTAAATCAGATCTGACACCAATGTGCGGTGTGAAACCAATTCACATT 188
QY 181 GTGGATTACAACTAAATGGAATCCAGATGACTATGCGGTGTGAAACCAATTCACATT 240
DB 189 GTGGATTACAACTAAATGGAATCCAGATGACTATGCGGTGTGAAACCAATTCACATT 248
QY 241 CCTTCAGAAAAGATCTGGCGCCAGACCTTGTCTCTATAACATGACAGATGGTGACTTT 300
DB 249 CCTTCAGAAAAGATCTGGCGCCAGACCTTGTCTCTATAACATGACAGATGGTGACTTT 308

Db 249 GTGATTACAACTTGAATGGAATCCAGATGACTATGAGAGGATGAAAAAATTCACATC 308
QY 241 CCTTCAGAAAAGATCTGGCCCGCAGACCTGTTCTCTATACAGATGACAGATGGTGAATTT 300
Db 309 CCCTCGAAAAGATCTGGCCCGCAGAGCTGTTCTCTATACAAACGACGAGCGGACTTT 368
QY 301 GCTATTGCTCAAGTTTCAACCAAGTCTCTCGAGTACACTGGCCACATCAGCTGGACACCT 360
Db 369 GCCATTGCTCAAAATTCACCAAGGTCTCTGGACTACACCGGCCACATCAGCTGGACACCG 428
QY 361 CCAGCCATCTTTAAAGCTACTGTGAGATCATGTCACCCACATTTCCCTTTGATGACAG 420
Db 429 CCAGCCATCTTTAAAGCTACTGTGAGATCATGTCACCTACTCTCCCTTCGATGAGCAG 488
QY 421 AACTGACGATGAAGCTGGGACCTGACCTAGACGCGCTGTGCTGGCCATCAACCCG 480
Db 489 AACTGACGATGAAGCTGGGACCTGACCTATGACGCGCTGTGCTGGGCCATTAACCCG 548
QY 481 GAAAGGACGACGACGACCTGAGCACTTCATGGAGAGCGGGAGTGGGTGATCAAGGAG 540
Db 549 GAAAGTGAACGACGCGGACCTGAGTAACCTTCATGGAGAGCGGGAGTGGGTGATCAAGGAA 608
QY 541 TCCCGGGCTGGAGCACTCCGTGACCTATTCTGCTGCCCGCAGACCCCTACCTGAC 600
Db 609 GCTCGGGCTGGAGCACTGGGTGTTCTACTCTGCTGCCCGCAGACCTCCCTACCTGGAC 668
QY 601 ATCACTTACCACCTGCTGATGACGCGCTG 630
Db 669 ATCACTTACCACCTGCTGATGACGCGCTG 698

RESULT 9

MUSACHRAB
LOCUS
DEFINITION Mus musculus acetylcholine receptor alpha-subunit mRNA, complete cds.
MI17640.1 GI:2073542
MUS musculus.
MUS musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1860)
Boulter, J., Luyten, W., Evans, K., Mason, P., Ballivet, M., Goldman, D., Stengelin, S., Martin, G., Heinemann, S. and Patrick, J.
Isolation of a clone coding for the alpha-subunit of a mouse acetylcholine receptor.
J. Neurosci. 5 (9), 2545-2552 (1985)
85292055
2993547
REFERENCE 2 (bases 1 to 1860)
Boulter, J.
Direct Submission
Submitted (08-MAY-1997) Psychiatry, UCLA, 760 Westwood Plaza, Los Angeles, CA 90095-1759, USA
sequence update
REMARK On May 8, 1997 this sequence version replaced gi:191601.
FEATURES
SOURCE
1. 1860
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="pBMA407"
/cell_line="BC-3-H-1"
105, 1478
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/protein_id="AAB53942.1"
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HREIVQVTLGLIQLINDEVNQIIVTINRLKQWVDYNLKNPDDYGGVKKIHIPS

CDS

1860 bp mRNA linear ROD 14-SEP-1999
R. norvegicus mRNA for acetylcholine receptor alpha-subunit.
X74832
X74832.1 GI:398831
acetylcholine receptor alpha.
Rattus norvegicus.
Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1849)
Witzemann, V., Stein, E., Barg, B., Konno, T., Koenen, M., Kues, W.,

EKIWRPDVLYNNADGDFALVKTGVLLDYTGHTTTPPAIFKSYCEIIVTHPPFDEQ
NCSMKLGTWTYDGSVAIINPDIISNFMESGEWIKERGMKHWYFSCPTTPY
LDITYHFVQRLPYIVNVIIPCLLSFLTSVLYFLDSDGKMTLSVLSLTVF
LLVIVELIPSTSAVPLIGKMLFTWVFIASIIIVIVINHRSPTSHIMPVVRK
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IELHGGH

BASE COUNT 448 a 498 c 436 g 478 t

ORIGIN

Query Match 83.5%; Score 526; DB 10; Length 1860;
Best Local Similarity 89.7%; Pred. No. 3e-112; Indels 0; Gaps 0;
Matches 565; Conservative 0; Mismatches 65;
QY 1 TCGAATGAGAGCCCGTCTGGTGGCAAGCTATTTAAAGACTACAGCAGCGTGGTCGG 60
Db 165 TCGAATGAGAGCGCTCTGGTGGCAAGCTCTTTGAAGACTACAGCAGGTAGTCCGG 224
QY 61 CCAGTGAAGACACCACCGGCTGAGAGTCAACCTGGCCCTGACGCTGATACAGCTC 120
Db 225 CCAGTGAAGACACCACCGTGGATTTACAAGTCAACCTGGCTCTACAGCTGATCCAGCTT 284
QY 121 ATCAATGTGATGAAGTAAATCAGATCGTGACAACCAATGTGCTCTGAAACACCAATGG 180
Db 285 ATCAATGTGATGAAGTAAATCAGATCGTGACAACCAATGTGCTCTGAAACACCAATGG 344
QY 181 GTGATTACAACTTAAATGGAATCCAGATGACTATGCGGTGTGAAAAAATTCACATT 240
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QY 241 CTTTCAGAAAAGATCTGGCCCGCAGACCTTGTCTCTATACGATGACAGTGGTGAATTT 300
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QY 361 CCAGCCATCTTTAAAGCTACTGTGAGATCATCGTCCACCTTCCCTTTGATGAACAG 420
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QY 421 AACTGACGATGAAGCTGGGACCTGACCTGACCTACGAGCTGTGCTGGCCATCAACCCG 480
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QY 481 GAAAGCACCAGCAGACCTGAGCACTTCATGAGAGCGGGAGTGGGTGATCAAGGAG 540
Db 645 GAAAGTGAACGACCGCCGACCTGAGTAACTTCATGAGAGCGGGAGTGGGTGATCAAGGAA 704
QY 541 TCCCGGGCTGGAGACACTCCGTGACCTATTCTGCTGCCCGCAGACCCCTACCTGAC 600
Db 705 GCTCGGGCTGGAGACACTGGTGTCTTACTCTGCTGCCCGCAGCCTCTCTACTCTGAC 764
QY 601 ATCACTTACCACCTGCTGATGACGCGCTG 630
Db 765 ATCACTTACCACCTGCTGATGACGCGCTG 794

RESULT 10

RNACRAL
LOCUS
DEFINITION R. norvegicus mRNA for acetylcholine receptor alpha-subunit.
X74832
X74832.1 GI:398831
acetylcholine receptor alpha.
Rattus norvegicus.
Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 1849)
Witzemann, V., Stein, E., Barg, B., Konno, T., Koenen, M., Kues, W.,


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/gene="nachral"
/product="alpha-1 subunit, nicotinic acetylcholine
receptor"
BASE COUNT      354 a      376 c      313 g      350 t
ORIGIN
Query Match      67.7%; Score 426.8; DB 5; Length 1393;
Best Local Similarity 79.8%; Pred. No. 4e-89;
Matches 503; Conservative 0; Mismatches 127; Indels 0; Caps 0;
QY 1 TCCGAACATGAGACCCCTCTGGTGGCAAGCTATTAAAGACTACAGCGGTGGTGGC 60
Db 64 TAGAGACAGAGAGCGCTGGTGGATGACCTGTTCGGGAATACAGCAAGGTGGTGGC 123
QY 61 CCAGTGAAGACACCCCGAGTGGTGGAGGTGACCGTGGCCGTGACGTGATACAGCTC 120
Db 124 CCGTGGAGAAATCACCGGATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 183
QY 121 ATCAATGTGATGAAGTAAATCAGATCGTGACAAACCAATGTCGTGAAACAGCAATGG 180
Db 184 ATCAATGTGATGAAGTAAATCAGATGTAACAAACCAATGTCGTGAAACAGCAATGG 243
QY 181 GTGATGTACAACTAAATGGAATCCAGATGACTATGCGCGTGTGAAAAAATTCACATT 240
Db 244 ACAGACATAAATGGAATGGAATCCAGATGACTGCGTGGTGAACAAATCCGATC 303
QY 241 CCTTCAGAAAGATGTCGGCCCGAGACCTGTTCTCTATTAACGATGAGATGAGCTTT 300
Db 304 CCATCAGACACATCTGGCCCGAGATCTTGTCTTTACAAACATGAGATGCGGATTT 363
QY 301 GCTATTGTCAGTTCACCAAGTGCCTCGACGTACACTGCGCCACATCAGTGGACACT 360
Db 364 GCCATTGTTAAATACCAAGTGCCTCTGGAACACACAGAAATACCTTGAGCCCT 423
QY 361 CCAGCCATCTTTAAAGCTACTGTGATGATCATGCTCACCCACTTCCCTTTGATGAACAG 420
Db 424 CCTGCTATCTTTAAAGTACTGTGAATATAGTCACGTACTTCCCATTCGATCAGCAG 483
QY 421 AACTGCAGATGAAGTGGGACCTGACCTGACCTAGACGGCTCTGCGGGCCATCAACCCG 480
Db 484 AACTGTAGCATGAAGTGGGAGGTGGACGTATGACGTATGAGTGGTGGTGGTGGTGG 543
QY 481 GAAAGCGACGACGACGACCTGAGCACTTCTGAGAGCGGGAGTGGTGGTGGTGGTGG 540
Db 544 GAGAGCGATCGCCCGACCTGAGTAACTTCTGAGAGCGGGTGGTGGTGGTGGTGGTGG 603
QY 541 TCCCGGGCTGGAGCACTCCGTGACCTATTCCTGCTGCCCGACACCCCTACCTGGAC 600
Db 604 TACCGTGGCTGGAGCACTGGGTTTACTACGCTGCTGCCCTGACACCCCTACCTGGAC 663
QY 601 ATCACTACCACTTGTGATGACGGCGCTG 630
Db 664 ATCACTACCACTTGTGATGACGGCGCTG 693

RESULT 12
FSCACHRA
LOCUS
DEFINITION
Ray (T.californica) acetylcholine receptor alpha subunit mRNA,
complete cds.
VERSION
J00963.1 GI:213217
KEYWORDS
acetylcholine receptor.
SOURCE
Ray (T.californica [1]; Torpedo marmorata [2],[4]) electric organ,
cDNA to mRNA.
ORGANISM
Torpedo californica
Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajae; Batoidae;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
REFERENCE
1 (bases 102 to 1191; 1207 to 1419)
AUTHORS
Sumikawa,K., Houghton,M., Smith,J.C., Bell,L., Richards,B.M. and
Barnard,E.A.
TITLE
The molecular cloning and characterisation of cDNA coding for the
```

```
alpha subunit of the acetylcholine receptor
Nucleic Acids Res. 10 (19), 5809-5822 (1982)
83064520
6183641
2 (bases 1 to 2045)
Noda,M., Takahashi,H., Tanabe,T., Toyosato,M., Furutani,Y.,
Hirose,T., Asai,M., Inayama,S., Miyata,T. and Numa,S.
Primary structure of alpha-subunit precursor of Torpedo californica
acetylcholine receptor deduced from cDNA sequence
Nature 299 (5886), 793-797 (1982)
83036943
6182472
3 (bases 124 to 1938)
Devillers-Thiery,A., Giraudat,J., Bentabollet,M. and Changeux,J.P.
Complete mRNA coding sequence of the acetylcholine binding
alpha-subunit of Torpedo marmorata acetylcholine receptor: a model
for the transmembrane organization of the polypeptide chain
Proc. Natl. Acad. Sci. U.S.A. 80 (7), 2067-2071 (1983)
83169822
6572962
4 (bases 1 to 2045)
Numa,S., Noda,M., Takahashi,H., Tanabe,T., Toyosato,M., Furutani,Y.
and Kikuyotani,S.
Molecular structure of the nicotinic acetylcholine receptor
Cold Spring Harb. Symp. Quant. Biol. 48 Pt 1, 57-69 (1983)
84206567
6586363
The alpha subunit for the acetylcholine receptor consists of 461
amino acids including a 24 amino acid prepeptide. This subunit is
thought to contain the acetylcholine binding site and [1] suggests
possible sites. Although the sequences [1] versus [2], [4] differ
at > twenty sites, this probably reflects species variation, since
all propose the same protein sequence with exception of the amino
acid residue 42 (site 383). [2] argues that the single mRNA species
forachr-alpha fails to cross-hybridize with the same mRNA from cat
muscle. [4] proposes a model for the transmembrane organization of
the alpha-subunit.
FEATURES
Location/Qualifiers
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/db_xref="taxon:7787"
103
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107
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127
/notes="c in [2],[4]; a in [1]"
187..1572
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FDQNCMTKLGITWYDGTGKVSIPESDPLSTFMESGEVWMDYRGKHWYITCCP
DTPYLDITTHFIMORIPLYFVNVIIPCLIFSLTGLVFLYPTDSDGKMTLSVLLS
LTVLLIVLVEIPSTSSAPLVKLYMLTFMIFVSIITVTVVINTHRRSPSTWPO
WVKRIFDITIPNVMTFTMKRASKENKIFADDIDISDICKQVGTGVIOTPLIK
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190..258
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213
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711
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735
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846
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variation
variation
variation
variation
variation
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variation 947 /note="t in [2],[4]; g in [1]"
variation 1129 /note="g in [2],[4]; a in [1]"
variation 1158 /note="c in [2],[4]; t in [1]"
variation 1210 /note="a in [2],[4]; g in [1]"
variation 1528 /note="t in [4], a in [1]"
variation 1620 /note="g in [4]; t in [1]"
variation 1697 .1698 /note="tta in [4]; ta in [1]"
variation 1738 .1739 /note="g in [4]; ag in [1]"
variation 1753 .1755 /note="atg in [4]; gta in [1]"
variation 1789 /note="a in [4]; g in [1]"
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variation 1808 /note="c in [4]; t in [1]"
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variation 1850 .1851 /note="ag in [4]; ca in [1]"
BASE COUNT 647 a 318 c 423 g 657 t
ORIGIN 112 bases upstream of BglII site ([Nature 299, 793-797 (1982)]).

Query Match 56.2%; Score 354; DB 5; Length 2045;
Best Local Similarity 72.8%; Pred. No. 3.9e-72;
Matches 456; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

Qy 1 TCCGAACATGAGACCCGCTCTGGTGCCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG 60
Db 259 TCTGAACATGAACACGTTGCTGCTAATTTATTAGAAAAATTAACAAGGTGATTGCT 318

Qy 61 CCAGTGGAGACCCCGCAGGTGCTGGAGCTACCCGTGGCGCTGCAGCTGATACAGTCT 120
Db 319 CCAGTGGAGCATCACCCACTTGTAGATATTACAGTGGGGCTACAGCTGATACACTC 378

Qy 121 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACTGTCGCTCTGAAACAGCAATGG 180
Db 379 ATCAGTGTGGATGAAGTAAATCAGATCGTGACAACTGTCGCTCTGAAACAGCAATGG 438

Qy 181 GTGGATTACAACCTAAATGGAATCCAGATGACTATGGCGGTGTGAAACAAATTCACATT 240
Db 439 ATTGATGTGAGGCTTCGGCTGGAAATCCAGCCGATTATGTTGGAATTAACAAAGATCAGACTG 498

Qy 241 CCTTCAGAAAAGATCTGGCGCCAGACCTTGTCTCTATAACGATGCAGATGGTGACTTT 300
Db 499 CCTTCGATGATGTTGGCTGCCAGATTAGTCTGTACAACTATGCTGATGGTGATTTT 558

Qy 301 GCTATTGTCAAGTTCACCAAAAGTGTCTCGAGTACACTGGCCACATCACCTGGACACT 360
Db 559 GCCATTGTCATGACCAAACTGCTTTGGATTATAGGGGAAAATTAATGTGACACT 618

Qy 361 CCAGCATCTTTAAAGCTACTGTGAGATCATCGTACCCACTTTCCCTTTGATGAACAG 420
Db 619 CCAGCAATCTTCAAAAGCTATTGTGAATTTATGTAACACATTTCCCATTTGATCAACAA 678

Qy 421 AACTGCAGCATGAAGCTGGCCACCTGGACCTACGACGCTCTGTCTGGCCATCAACCCG 480
Db 679 AATTGCATGAAGTGGGAATCTGGACGTACCATGGGACAAAAGTTTCCATATCCCCG 738

Qy 481 GAAAGCAGCAGCAGCTGAGCAACTTTCATGGAGAGCGGGAGTGGGTGATCAAGAG 540
Db 739 GAAAGTACCGTCCGGATCTCAGTACATTTATGAAAGTGGAGAGTGGGTAAAGAGAT 798

Qy 541 TCCCGGGCTGGAAGACACTCCGTGACCTATTCTCTGCCGACACACCCCTACCTGGAC 600
Db 799 TATCGTGGATGAAGCACTGGGTGATTATACCTGCTCCTGACACTCCTTACCTGGAT 858

Qy 601 ATCAGCTACCACTTCGTATGACGCG 626
Db 859 ATCAGCTACCACTTTATCATGACGCG 884

RESULT 13
AR106255 AR106255 1350 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6106840.
DEFINITION AR106255
ACCESSION AR106255
VERSION AR106255.1 GI:12820785
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1350)
AUTHORS Clark, B.R., Sharma, S.D. and Lerch, B.L.
TITLE MHC conjugates useful in ameliorating autoimmunity
JOURNAL Patent: US 6106840-A 1 22-AUG-2000;
FEATURES Location/Qualifiers
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BASE COUNT 384 a 241 c 287 g 438 t
ORIGIN

Query Match 55.7%; Score 350.8; DB 6; Length 1350;
Best Local Similarity 72.5%; Pred. No. 2.1e-71;
Matches 454; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 1 TCCGAACATGAGACCCGCTCTGGTGCCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG 60
Db 37 TCTGAACATGAAGACGTTGCTGCTAATTTATTAGAAAAATTAACAAGGTGATTGCT 96

Qy 61 CCAGTGGAGACCCCGCAGGTGCTGGAGGTACCGTGGCGCTGCAGTGTATACAGTCT 120
Db 97 CCAGTGGAGCATCACCCACTTTGTAGATATTACAGTGGGGCTACAGCTGATACACTC 156

Qy 121 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACTATGCGTCTGAAACAGCAATGG 180
Db 157 ATCAGTGTGGATGAAGTAAATCAGATCGTGACAACTATGCGCTTAAGCGCAATGG 216

Qy 181 GTGGATTACAACCTAAATGGAATCCAGATGACTATGGCGGTGTGAAACAAATTCACATT 240
Db 217 ATTGATGTGAGGCTTCGGCTGGAAATCCAGCCGATTATGTTGGAATTAACAAAGATCAGACTG 276

Qy 241 CCTTCAGAAAAGATCTGGCGCCAGACCTTGTCTCTATAACGATGCAGATGGTGACTTT 300
Db 277 CCTTCGATGATGTTGGCTGCCAGATTAGTCTGTACAAAGATGCTGATGGTGATTTT 336

Qy 301 GCTATTGTCAAGTTCACCAAAAGTGTCTCGAGTACACTGGCCACATCACCTGGACACT 360
Db 337 GCCATTGTTCATGACCAAACTGCTTTGGATTATACGGGAAAATTAATGTGGACACT 396

Qy 361 CCAGCATCTTTAAAGCTACTGTGAGATCATCGTACCCACTTTCCCTTTGATGAACAG 420
Db 397 CCAGCAATCTTCAAAAGCTATTGTGAATTTATGTAACACATTTCCCATTTGATCAACAA 456

Qy 421 AACTGCAGCATGAAGCTGGCCACCTGGACCTACGACGCTCTGTCTGGCCATCAACCCG 480
Db 457 AATTGCATGATGAAGTGGGAATCTGGACGTACGATGGGACAAAAGTTTCCATATCCCG 516

Qy 481 GAAAGCAGCAGCAGCTGAGCAACTTTCATGGAGAGCGGGAGTGGGTGATCAAGAG 540
Db 517 GAAAGTACCGTCCGGATCTCAGTACATTTATGGAAGTGGAGAGTGGGTAAAGAGAT 576

Qy 541 TCCCGGGCTGGAAGACACTCCGTGACCTATTCTCTGCCGACACACCCCTACCTGGAC 600
Db 577 TATCGTGGATGAAGCACTGGGTGATTATTACCTGCTCTGACACTCCTTACCTGGAT 636

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Qy 601 ATCACCTACCACTTCGTCATGCAGCG 626
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Db 637 ATCACCTACCACTTCGTCATGCAGCG 662

RESULT 14
FSCACHR 1815 bp mRNA linear VRT 11-APR-1996
LOCUS T.marmorata acetylcholine receptor alpha-subunit mRNA, complete
DEFINITION
ACCESSION M25893
VERSION M25893.1 GI:213215
KEYWORDS acetylcholine receptor.
SOURCE T.marmorata electric organ, cDNA to mRNA.
ORGANISM Torpedo marmorata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiogaster; Batoidae;
Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
REFERENCE 1 (bases 1 to 1815)
AUTHORS Devillers-Thiery,A., Giraudat,J., Bentabollet,M. and Changeux,J.P.
TITLE Complete mRNA coding sequence of the acetylcholine binding
alpha-subunit of Torpedo marmorata acetylcholine receptor: a model
for the transmembrane organization of the polypeptide chain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (7), 2067-2071 (1983)
MEDLINE 83169822
PUBMED 6572962
REFERENCE 2 (bases 1 to 1815)
AUTHORS Devillers-Thiery,A., Giraudat,J., Bentabollet,M., Klarsfeld,A. and
Changeux,J.P.
TITLE Molecular genetics of Torpedo marmorata acetylcholine receptor
JOURNAL Adv. Exp. Med. Biol. 181, 17-29 (1984)
MEDLINE 85171452
PUBMED 6549423
FEATURES
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1..1815
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/db_xref="taxon:7798"
64..1449
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BASE COUNT 563 a 287 c 378 g 587 t
ORIGIN

Query Match 55.7%; Score 350.8; DB 5; Length 1815;
Best Local Similarity 72.5%; Pred. No. 2.2e-71;
Matches 454; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 1 TCCGAACATGAGACCGCTCTGGTGGCAAGACTATTTAAAGACTACAGCGGTGGCGG 60
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Db 136 TCTGACATGAACACGCTTTGGTGTCTTAATTTATAGAAATTAACACAGGTATTCGT 195
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Qy 61 CCAGTGAAGACACCCCGAGGTCTGGAGGTCCACCGTGGCCCTGACGCTGATACAGCTC 120
|||||
Db 196 CCAGTGGAGCATCACACCCACTTGTAGATATTACAGTGGGCTACAGCTGATACACTC 255
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Qy 121 ATCAATGTGATGAAGTAATAGATCGTGCACACCAATAGTGCCTGTAACACCAATGG 180
|||||
Db 256 ATCAATGTGATGAAGTAATAGATCGTGCACACCAATAGTGCCTGTAACACCAATGG 315
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Qy 181 GTGATTACACCTAAATCCAGATCACTATCGCGGTGTGAAAAAATTCACATT 240
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Db 316 ATTGATGTGAGGCTTCGCTGAATCCAGCGGATATGTTGGAATTAATAAAGATCAGACTG 375
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sig_peptide 40.99
mat_peptide 100.1410
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Query Match		55.2%	Score 348;	DB 5;	Length 1421;
Best Local Similarity		72.1%	Pred. No. 9,6e-71;		
Matches 453;		Conservative 0;	Mismatches 175;	Indels 0;	Gaps 0;
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QY	62	CAGTGGAGACACCGCCAGGTCGTTGGAGGTCAACCGTGGGCCGTGAGCTGATACAGCTCA	121		
QY	161	CTGTAGAACATATAAGGATCAAGTAGTGGTAACCTGTTGGACTTCAGCTCATCCAGCTCA	220		
QY	122	TCAATGTGGATGAAGTAAATCAATCAGTCTGCACACCAATGTGGTCTGAAACAGCAATGG	181		
Db	221	TCACGTGGATGAAGTGAACCAATGTGTTCAACAAATATCCGCCATAAACAGCAATGGC	280		
QY	182	TGGATTACAACCTAAATGGATCCAGATGACTATGGGGTGTGAAAGAAATTCACATTC	241		
Db	281	GTGATGTTAACTCAAGTGGGACCCAGCAAAATATGGCGGTAAAGAAATTCGAATTC	340		
QY	242	CTTCAGAAAGATCTGGGCCCGACACCTTGTTCTCTATAACGATGCAGATGGTGACTTTG	301		
Db	341	CTTCCAGTGACGTTTGGAGTCCAGATTTGGTTCTTTATAACAATGCAGATGGTGACTTTG	400		
QY	302	CTATTGTCAAGTTCAACAAAGTGCCTCGCAGTACACTGGCCACATCAGTGGACACCTC	361		
Db	401	CTATTTCAGAGACACTAAATCCTCTGGATACACTGGAAAGATTACATGGACACCCC	460		
QY	362	CAGCCATCTTTAAAGCTACTGTGAGATCATGTCACCCACCTTCCCTTTTGATGAACAGA	421		
Db	461	CAGCAATTTTCAAAAGCTACTGTGAAATCATAGTCACATACTTCCGTTTGATCAGCAGA	520		
QY	422	ACTGCAGCATGAGCTGGCCACCTGGACCTAGCAGCGCTCTGCTGGCCATCAACCCGG	481		
Db	521	ATTGCAGCATGAAGTTTGGCACTTGGACTTATGATGGAGCTTACTAGTTATAATCCAG	580		
QY	482	AAAGCGACCGACGACCTGAGCAACTTCATGGAGAGCGGGAGTGGGTGATCAAGGAGT	541		
QY	581	AGAGGACCGACCGACGATCTGAGCAACTTCATGGCGGAGTGGAGATGGATGAAGGACT	640		
QY	542	CCCGGGCTGGAAGCACTCCGTGACTATTCTGTCGCCCGACACCCCTACCTGGACA	601		
Db	641	ATCGTTGCTGGAAGCATTTGGGTTTATTATACCTGTTGCCAGATAAACCATATCTGGATA	700		
QY	602	TCACCTACGACTTCGTCATGAGCGCCT	629		
Db	701	TCACCTACGACTTTGTTCTCAAAAGGCT	728		

Search completed: January 14, 2003, 16:10:36
Job time : 3123 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 16:53:48 ; Search time 36 Seconds
(without alignments)
171.634 Million cell updates/sec

Title: US-09-820-339a-2
Perfect score: 1143
Sequence: 1 SEHETRLVAKLFKDYSSVVR.....SCCPDTPYLDITYHFVQMRL 210

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1096	95.9	457	1	US-08-278-635B-3
2	1096	95.9	457	3	US-08-471-961-3
3	1096	95.9	458	3	US-08-464-258B-3
4	898	78.6	449	3	US-08-462-351-2
5	898	78.6	449	4	US-09-602-807-2
6	896	78.4	449	6	5468481-1
7	888	77.7	449	6	5194425-1
8	597.5	52.3	504	4	US-08-487-596-4
9	595.5	52.1	504	2	US-08-466-589-4
10	595.5	52.1	504	2	US-08-700-636-4
11	595.5	52.1	504	3	US-08-467-574-4
12	595.5	52.1	504	4	US-09-217-345-4
13	594.5	52.0	497	1	US-08-278-635B-5
14	594.5	52.0	497	3	US-08-464-258B-5
15	594.5	52.0	497	3	US-08-471-961-5
16	582.5	51.0	629	1	US-08-278-635B-6
17	582.5	51.0	629	3	US-08-464-258B-6
18	582.5	51.0	629	3	US-08-471-961-6
19	576	50.4	468	4	US-08-487-596-8
20	575.5	50.3	529	1	US-08-496-855A-2
21	575.5	50.3	529	4	US-08-487-596-2
22	569.5	49.8	494	4	US-08-487-596-10
23	567.5	49.7	510	1	US-08-278-635B-4
24	567.5	49.7	510	3	US-08-471-961-4
25	564.5	49.4	511	3	US-08-464-258B-4
26	549	48.0	528	2	US-08-466-589-2
27	549	48.0	528	2	US-08-700-636-2

28	549	48.0	528	3	US-08-467-574-2	Sequence 2, Appl1
29	549	48.0	528	4	US-09-217-345-2	Sequence 2, Appl1
30	548.5	48.0	627	2	US-08-466-589-6	Sequence 6, Appl1
31	548.5	48.0	627	3	US-08-700-636-6	Sequence 6, Appl1
32	548.5	48.0	627	3	US-08-467-574-6	Sequence 6, Appl1
33	548.5	48.0	627	4	US-09-217-345-6	Sequence 6, Appl1
34	547.5	47.9	627	4	US-08-487-596-6	Sequence 6, Appl1
35	536.5	46.9	458	4	US-08-487-596-16	Sequence 16, Appl1
36	472	41.3	502	1	US-08-496-855A-4	Sequence 4, Appl1
37	472	41.3	502	2	US-08-466-589-10	Sequence 10, Appl1
38	472	41.3	502	3	US-08-700-636-10	Sequence 10, Appl1
39	472	41.3	502	3	US-08-467-574-10	Sequence 10, Appl1
40	472	41.3	502	4	US-09-217-345-10	Sequence 10, Appl1
41	472	41.3	502	4	US-08-487-596-14	Sequence 14, Appl1
42	469.5	41.1	479	1	US-08-278-635B-2	Sequence 2, Appl1
43	469.5	41.1	479	3	US-08-464-258B-2	Sequence 2, Appl1
44	469.5	41.1	479	3	US-08-471-961-2	Sequence 2, Appl1
45	456	39.9	498	1	US-08-496-855A-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-278-635B-3
; Sequence 3, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,635B
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-278-635B-3

Query Match 95.9%; Score 1096; DB 1; Length 457;
Best Local Similarity 94.8%; Pred. No. 1.6e-112;
Matches 199; Conservative 6; Mismatches 5; Indels 0; Caps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIYTTNRLKQW 60
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DB 21 SEHETRLVAKLFEDYSSVVRPVEDHREIVQVTGVLQIQLINVDENVQIYTTNRLKQW 80
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QY 61 VDYNLKNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGFAIVKFTKVLQYTGHTITWP 120
DB 81 VDYNLKNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGFAIVKFTKVLQYTGHTITWP 140
QY 121 PAIFKSYCEIIVTHFPFDEQNCMKLGTWTYD-INTESQDPLSNFMESGEWIK 180
DB 141 PAIFKSYCEIIVTHFPFDEQNCMKLGTWTYD-INTESQDPLSNFMESGEWIK 180
QY 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
DB 201 ARGKWHWFYSCCPTTPYLDITYHFVMQRL 230

RESULT 2
US-08-471-961-3
; Sequence 3, Application US/084.1961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-471-961-3
Query Match 95.9%; Score 1096; DB 3; Length 457;
Best Local Similarity 94.8%; Pred. No. 1.6e-112;
Matches 199; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
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DB 21 SEHETRLVAKLFEDYSSVVRPVEDHREIVQVTVGLQIQLINVDENVQIVTTNVRLLKQOW 80
QY 61 VDYNLKNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGFAIVKFTKVLQYTGHTITWP 120
DB 81 VDYNLKNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGFAIVKFTKVLQYTGHTITWP 140
QY 121 PAIFKSYCEIIVTHFPFDEQNCMKLGTWTYDGSVVAINPESQDPLSNFMESGEWIK 180
DB 141 PAIFKSYCEIIVTHFPFDEQNCMKLGTWTYDGSVVAINPESQDPLSNFMESGEWIK 180
QY 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
DB 201 ARGKWHWFYSCCPTTPYLDITYHFVMQRL 230

US-08-471-961-3
Query Match 95.9%; Score 1096; DB 3; Length 457;
Best Local Similarity 94.8%; Pred. No. 1.6e-112;
Matches 199; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTTNVRLLKQOW 60
DB 21 SEHETRLVAKLFEDYSSVVRPVEDHREIVQVTVGLQIQLINVDENVQIVTTNVRLLKQOW 80
QY 61 VDYNLKNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGFAIVKFTKVLQYTGHTITWP 120
DB 81 VDYNLKNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGFAIVKFTKVLQYTGHTITWP 140
QY 121 PAIFKSYCEIIVTHFPFDEQNCMKLGTWTYDGSVVAINPESQDPLSNFMESGEWIK 180
DB 141 PAIFKSYCEIIVTHFPFDEQNCMKLGTWTYDGSVVAINPESQDPLSNFMESGEWIK 180
QY 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
DB 201 ARGKWHWFYSCCPTTPYLDITYHFVMQRL 230

DB 141 PAIFKSYCEIIVTHFPFDEQNCMKLGTWTYDGSVVAINPESQDPLSNFMESGEWIK 200
QY 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
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RESULT 3
US-08-464-258B-3
; Sequence 3, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-464-258B-3
Query Match 95.9%; Score 1096; DB 3; Length 458;
Best Local Similarity 94.8%; Pred. No. 1.6e-112;
Matches 199; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTTNVRLLKQOW 60
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Query Match	78.6%	Score 898	DB 3	Length 449	0
Best Local Similarity	74.3%	Pred. No. 1e-90			0
Matches 156	Conservative 26	Mismatches 28	Indels 0	Gaps 0	
QY	1	SEHETRLVAKLFKDYSSVWRPVEDHROVQEVYTAGLQIQLINDEVNOIVTNTVRLRQOW	60		
		: : : :			
Db	13	SEHERLVANLEENYKNVIRPVEHHTFVDITVGLQIQLISVDEVNOIVETNVLRLQOW	72		
		: : :			
QY	61	VDYLNKNPDDYGVKKIHIHPSEKILWRPDLVLYNNADGFAIVKTKVLLQVTHITWTP	120		
		: : : : : : : :			
Db	73	IDVLRWNPADYGGIKTIRLPSDDVWLPDLVLYKNADGFAIVHMTKLLDYTGKIMTP	132		
		: : : : : : : :			
QY	121	PAIFSKYCEIITVTHFPDQCSMKLGTWTYDGSVVAINPESDQDLSNFMESGEWJKE	180		
		: : : : : : : :			
Db	133	PAIFSKYCEIITVTHFPDQCNCTMKLGTWYDGTGKVSIPESDRDPLDTLFMESGEWVAKD	192		
		: : : : : : : :			
QY	181	SRGKHKHSYTVSCCPDTPYLDITYHFVQRQL	210		

QY 181 SRGKHSVYSCCPDTPYLDITYHFVMOQL 210
Db 193 YRGKHWVYTCPPDTPYLDITYHFIMORI 222

RESULT 6

5468481-1

; Patent No. 5468481

; APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L.

; IN AMELIORATING AUTOIMMUNITY

; NUMBER OF SEQUENCES: 7

; CURRENT APPLICATION DATA:

; FILING DATE: 14-APR-1992

; APPLICATION NUMBER: 690,840

; FILING DATE: 23-APR-1991

; APPLICATION NUMBER: 576,084

; FILING DATE: 30-AUG-1990

; APPLICATION NUMBER: 210,594

; FILING DATE: 23-JUN-1988

; APPLICATION NUMBER: 635,840

; FILING DATE: 28-DEC-1998

; APPLICATION NUMBER: 367,751

; FILING DATE: 21-JUN-1989

; SEQ ID NO:1:

; LENGTH: 449

5468481-1

Query Match

Best Local Similarity 78.4%; Score 896; DB 6; Length 449;

Matches 156; Conservative 26; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDVNOIYVTTNVLKQOW 60

Db 13 SEHETRLVANLLENKVRPVEHHTFVDITVGLQIQLISVDEVNOIYVETNVLKQOW 72

QY 61 VDYNLKWNPDYGGVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 120

Db 73 IDVLRWNPADYGGIKIRLPDSDVWLPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 132

QY 121 PAIFKSYCEIIVTHFPFDEQNGSMKLGITWYDGSVVAINPESDQDPLSNFMESEGEWVKE 180

Db 133 PAIFKSYCEIIVTHFPFDEQNGSMKLGITWYDGSVVAINPESDQDPLSNFMESEGEWVKE 192

QY 181 SRGKHSVYSCCPDTPYLDITYHFVMOQL 210

Db 193 YRGKHWVYTCPPDTPYLDITYHFIMORI 222

RESULT 7

54425-1

; Patent No. 5194425

; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,

; AMELIORATING AUTOIMMUNITY

; NUMBER OF SEQUENCES: 9

; CURRENT APPLICATION DATA:

; FILING DATE: 21-JUN-1989

; APPLICATION NUMBER: 210,594

; FILING DATE: 23-JUN-1988

; SEQ ID NO:1:

; LENGTH: 449

5194425-1

Query Match

Best Local Similarity 77.7%; Score 888; DB 6; Length 449;

Matches 155; Conservative 28; Mismatches 27; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDVNOIYVTTNVLKQOW 60

Db 13 SEHETRLVANLLENKVRPVEHHTFVDITVGLQIQLISVDEVNOIYVETNVLKQOW 72

QY 61 VDYNLKWNPDYGGVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 120

Db 73 IDVLRWNPADYGGIKIRLPDSDVWLPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 132

QY 121 PAIFKSYCEIIVTHFPFDEQNGSMKLGITWYDGSVVAINPESDQDPLSNFMESEGEWVKE 180

Db 133 PAIFKSYCEIIVTHFPFDEQNGSMKLGITWYDGSVVAINPESDQDPLSNFMESEGEWVKE 192

QY 181 SRGKHSVYSCCPDTPYLDITYHFVMOQL 210

Db 193 YRGKHWVYTCPPDTPYLDITYHFIMORI 222

RESULT 7

54425-1

; Patent No. 5194425

; APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,

; AMELIORATING AUTOIMMUNITY

; NUMBER OF SEQUENCES: 9

; CURRENT APPLICATION DATA:

; FILING DATE: 21-JUN-1989

; APPLICATION NUMBER: 210,594

; FILING DATE: 23-JUN-1988

; SEQ ID NO:1:

; LENGTH: 449

5194425-1

Query Match

Best Local Similarity 77.7%; Score 888; DB 6; Length 449;

Matches 155; Conservative 28; Mismatches 27; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDVNOIYVTTNVLKQOW 60

Db 13 SEHETRLVANLLENKVRPVEHHTFVDITVGLQIQLISVDEVNOIYVETNVLKQOW 72

QY 61 VDYNLKWNPDYGGVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 120

Db 73 IDVLRWNPADYGGIKIRLPDSDVWLPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 132

QY 121 PAIFKSYCEIIVTHFPFDEQNGSMKLGITWYDGSVVAINPESDQDPLSNFMESEGEWVKE 180

Db 133 PAIFKSYCEIIVTHFPFDEQNGSMKLGITWYDGSVVAINPESDQDPLSNFMESEGEWVKE 192

QY 181 SRGKHSVYSCCPDTPYLDITYHFVMOQL 210

Db 193 YRGKHWVYTCPPDTPYLDITYHFIMORI 222

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDVNOIYVTTNVLKQOW 60
Db 13 SEHETRLVANLLENKVRPVEHHTFVDITVGLQIQLISVDEVNOIYVETNVLKQOW 72
QY 61 VDYNLKWNPDYGGVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 120
Db 73 IDVLRWNPADYGGIKIRLPDSDVWLPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 132
QY 121 PAIFKSYCEIIVTHFPFDEQNGSMKLGITWYDGSVVAINPESDQDPLSNFMESEGEWVKE 180
Db 133 PAIFKSYCEIIVTHFPFDEQNGSMKLGITWYDGSVVAINPESDQDPLSNFMESEGEWVKE 192
QY 181 SRGKHSVYSCCPDTPYLDITYHFVMOQL 210
Db 193 YRGKHWVYTCPPDTPYLDITYHFIMORI 222

RESULT 8

US-08-487-596-4

; Sequence 4, Application US/08487596

; Patent No. 6440681

; GENERAL INFORMATION:

; APPLICANT: Elliot, Kathryn J.

; APPLICANT: Ellis, Steven B.

; TITLE OF INVENTION: Harpold, Michael M.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND

; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; APPLICATION NUMBER: WO US94/02447

; FILING DATE: 08-MAR-1994

; APPLICATION NUMBER: US 08/149,503

; FILING DATE: 08-NOV-1993

; APPLICATION DATA:

; FILING DATE: 08-MAR-1993

; APPLICATION NUMBER: US 07/938,154

; FILING DATE: 30-NOV-1992

; APPLICATION DATA:

; FILING DATE: 03-APR-1990

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; TELECOMMUNICATION INFORMATION: 6362-9951

; TELEPHONE: 619-238-0062

; TELEFAX: 619-238-0062

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 504 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

QY 61 VDNKLNWPNDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
DB 91 XDYKLNWPNDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
QY 121 PAIFKSSCKIDYTFPPDYQNCMTKFGSDYKAKIDLVLGSSMNLKDYWESGEWAIK 210
DB 151 PAIFKSSCKIDYTFPPDYQNCMTKFGSDYKAKIDLVLGSSMNLKDYWESGEWAIK 210
QY 181 SRGKHSVYSCCPDTPYLDITYHFVMORL 210
DB 211 APGYNHDIKYNCCEI-YPDITYSLIIRL 239

RESULT 11

US-08-467-574-4
; Sequence 4, Application US/08467574
; Patent No. 6022704
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,574
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9949
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-467-574-4

Query Match 52.1%; Score 595.5; DB 3; Length 504;
Best Local Similarity 50.5%; Pred. No. 2.8e-57;
Matches 106; Conservative 42; Mismatches 61; Indels 1; Gaps 1;
QY 1 SEHETRLVAKLFKDYSSVRPVEDHROQVVEVTAGLQLIQLINDEVNQIVTNNVRLKQOW 60
DB 31 SEAEHLRFLERLFEDYNEIRPVANVSDPVIHFVMSQLVKVDEVNQIMETNLWLKQIW 90
QY 61 VDNKLNWPNDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
DB 91 XDYKLNWPNDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
QY 121 PAIFKSSCKIDYTFPPDYQNCMTKFGSDYKAKIDLVLGSSMNLKDYWESGEWAIK 210

DB 151 PAIFKSSCKIDYTFPPDYQNCMTKFGSDYKAKIDLVLGSSMNLKDYWESGEWAIK 210
QY 181 SRGKHSVYSCCPDTPYLDITYHFVMORL 210
DB 211 APGYNHDIKYNCCEI-YPDITYSLIIRL 239

RESULT 12

US-09-217-345-4
; Sequence 4, Application US/09217345
; Patent No. 6303753
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-217-345-4

Query Match 52.1%; Score 595.5; DB 4; Length 504;
Best Local Similarity 50.5%; Pred. No. 2.8e-57;
Matches 106; Conservative 42; Mismatches 61; Indels 1; Gaps 1;
QY 1 SEHETRLVAKLFKDYSSVRPVEDHROQVVEVTAGLQLIQLINDEVNQIVTNNVRLKQOW 60
DB 31 SEAEHLRFLERLFEDYNEIRPVANVSDPVIHFVMSQLVKVDEVNQIMETNLWLKQIW 90
QY 61 VDNKLNWPNDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
DB 91 XDYKLNWPNDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
QY 121 PAIFKSSCKIDYTFPPDYQNCMTKFGSDYKAKIDLVLGSSMNLKDYWESGEWAIK 210

Wed Jan 15 08:40:24 2003

[illegible]

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RESULT 13
US-08-278-635B-5
; Sequence 5, Application US/08278635B
; Patent No. 5683912
; GENERAL INFORMATION:
; APPLICANT: ELGOVHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY KAT WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: F41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-278-635B-5
Query Match 52.0%; Score 594.5; DB 1; Length 497;
Best Local Similarity 51.4%; Pred. No. 3.6e-57;
Matches 108; Conservative 39; Mismatches 62; Indels 1; Gaps 1;

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US-08-464-258B-5
; Sequence 5, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOIHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8

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CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US - 08 - 464 - 258B - 5

Query Match          52.08;   Score 594.5;   DB 3;   Length 497;
Best Local Similarity 51.4%;   Pred. No. 3.6e-57;
Matches 108; Conservative 39; Mismatches 62; Indels 1; Gaps 1;

Qy      1 SEHEPRLVAKLFKDYSSVRPVEDHRQVVETAGLQLQLINVDVNQIVTNNVLKKQW 60
       || | | | | : : : : | : : : | : : : | : : : | : : : | : : |
Db      24 SEAEHRLFQYLFDEYNIEIRPVANYSHPIQFEVSMSQLVKVDVNMIMETNLWLKIW 83
       || | | | | : : : : | : : : | : : : | : : : | : : : | : : |

Qy      61 VDNLNKNPPDDYGKVKKTHIPSEKLWRPDVLVLYNNAADGFAIVKFKTVLLQYTGHITWP 120
       || | | | | : : : : | : : : | : : : | : : : | : : : | : : |
Db      84 NDYLKUKWPSDTQGVGEFRMRVPAEKLWKDPDLVLYNNAADGFQVDDKTALKKTIGVTWIP 143
       || | | | | : : : : | : : : | : : : | : : : | : : : | : : |

Qy     121 PAIFKSYCEIITHPPFPDQCNSCKMLGTWTYDGVSVAINPENSDQPDLSNFMESGEWIKE 180
       . | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     144 PAIFKSSCKIDTYTFPDFYQNCTMFKGWSYDKAKIDLVLIGSSMNLDKYDWESGEWAIIK 203
       . | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy     181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
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Db    204 APGYEHKEIKNCCEEI-YQDITYSLYIRRL 232

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RESULT 15
US-08-471-961-5
; Sequence 5, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.

Query Match	52.0%	Score 594, 5;	DB 3;	Length 497;
Best Local Similarity	51.4%	Pred. No. 3.6e-57;		
Matches 108; Conservative	39;	Mismatches 62;	Indels 1;	Gaps 1;
Qy	1	SEHETRLVAKLFKDYSVVVRVEDHQRVQVETAGLQLQLINVDENVQIVTNVRLKQOW	60	
Db	24	SEAEHRLFQYLFEDYNEILRPVAVNSHPVITQFEVSMSQLVKVDEVQIMETNLWLAKQIW	83	
Qy	61	VDYLNKNPDDYGGVKKIHIPSEKIRWPDVLVLYNNADGDFALYKFTKVLQYTGHTWTP	120	
Db	84	NDYKLLKWKPSDYOGVEFMRVPAEKIRWPDVLVLYNNADGDFQVDDKTKALLKYTGVTWIP	143	
	121	PAIFKSYCEIIVTHFFDEQNCMSKLGKWTYDGSVAINPESQDPLSNFMESGEVWIK	180	
Db	144	PAIFKSSCKIDVITYFPDQNTKFGWSYDKAKIDLVLIGSSMNLKDYWESGEWAIK	203	
Qy	181	SRGWKISVYSCCPDPYLDITYHFVMQRL	210	
Db	204	APCYKHEIKNCEEI-YQDITYSYIRL	232	

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Job time : 38 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 12:20:37 ; Search time 300 Seconds
(without alignments)
4729.196 Million cell updates/sec

Title: US-09-820-339A-1
Perfect score: 630
Sequence: 1 tccgaacatgagaccctct.....acttgctatgcagcgctg 630

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
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11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
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16: /SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
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18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
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22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	628.4	99.7	1667	21	Human acetylcholin
2	564.4	89.6	3649	6	Calf acetyl cholin
3	545	86.5	705	19	Human acetylcholin
4	530	84.1	690	19	Human acetylcholin
5	363	57.6	363	19	Human acetylcholin
6	354	56.2	1350	17	Acetylcholine rece
7	353.6	56.1	1350	14	Acetylcholine rece
8	352.4	55.9	1350	14	Alpha subunit of T
9	326.6	51.8	1350	15	Acetylcholine rece

10	278	44.1	438	19	AAV72832	Human acetylcholin
11	267	42.4	267	19	AAV72833	Human acetylcholin
12	224.2	35.6	2277	15	AAV12199	Human neuronal nic
13	224.2	35.6	2277	16	AAQ90387	Alpha 2 subunit of
14	224.2	35.6	2664	18	AAT48235	Neuronal nicotinic
15	224.2	35.6	2664	24	ABK92165	Prostate cancer-as
16	223.6	35.5	1908	18	AAT48236	Neuronal nicotinic
17	223.2	35.4	1757	15	AAV12200	Human neuronal nic
18	217.8	34.6	2082	18	AAT59527	Alpha4 subunit of
19	217.8	34.6	2082	18	AAT59528	Alpha4 subunit of
20	217.8	34.6	3496	18	AAT48237	Neuronal nicotinic
21	216.2	34.3	1809	23	AA591552	DNA encoding novel
22	208.2	33.0	2363	15	AAV12196	Human neuronal nic
23	200.2	31.8	4708	6	AA50415	Human acetyl choli
24	193.8	30.8	1869	24	AAAL45873	Modified acetylcho
25	193.8	30.8	1869	24	ABL54794	Modified hen ACR s
26	184.4	29.3	2210	23	ABL10275	Drosophila melanog
27	182.6	29.0	2385	23	ABL11821	Drosophila melanog
28	179.8	28.5	1743	18	AAT48232	Neuronal nicotinic
29	179.2	28.4	1509	22	AA515343	Human CHRN2 codin
30	179.2	28.4	1771	24	AAAD26345	Human mutant neuro
31	179.2	28.4	2448	15	AAV12201	Human neuronal nic
32	179.2	28.4	2448	18	AAT48240	Neuronal nicotinic
33	178	28.3	1377	22	AAAD20828	Human CHRN3 gene
34	178	28.3	1925	18	AAT48234	Neuronal nicotinic
35	177.6	28.2	1521	12	AAQ14288	Human neuronal nic
36	176.2	28.0	1869	24	AAAL45864	Modified acetylcho
37	176.2	28.0	1869	24	ABL54788	Insect nicotinic A
38	175.6	27.9	1938	17	AAQ99348	Alpha-9 nicotinic
39	173.4	27.5	1828	18	AAT48238	Neuronal nicotinic
40	173.2	27.5	2319	23	ABL04391	Drosophila melanog
41	168.4	26.7	1677	24	AAAD33651	Human TRICH-6 cDNA
42	168.4	26.7	1932	22	AAAD03528	Human nicotinic ac
43	167	26.5	1896	24	AAAL45870	Modified acetylcho
44	167	26.5	1896	24	ABL54791	Modified hen ACR s
45	166.8	26.5	1299	22	AA501279	Mature alpha nicot

ALIGNMENTS

RESULT 1
AAZ38821
ID AAZ38821 standard; cDNA; 1667 BP.
XX
AC AAZ38821;
XX
DT 14-FEB-2000 (first entry)
XX
DE Human acetylcholine receptor nucleotide sequence.

XX
KW Human; acetylcholine receptor; AChR; immune response; allergy;
KW antibody-mediated disease; gene replacement therapy; T cell epitope;
KW dermatological; immunosuppressive; antiinflammatory; haemostatic;
KW antianemic; antiallergic; antidiabetic; antithyroid; antidiabetic;
KW autoimmune disease; allergic disease; ss.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 49..1422
FT /tag= a
FT /product= "acetylcholine receptor"

XX
PN WO9930736-A2.
XX
PD 24-JUN-1999.
XX
PF 16-DEC-1998; 98WO-US26787.
XX
PR 16-DEC-1997; 97US-0991143.
XX
PA (MINU) UNIV MINNESOTA.


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QY 241 CCTTCAAAAGATCTGGCCGACAGACCTGTTCTCTATACGATGAGATGGTACTTT 300
DB 347 CCTTCGAAAAGATCTGGCCGACAGACCTGTTCTTTATAACATGAGATGGTACTTT 406
QY 301 GCTATTGCTCAAGTTACAAAAGTCTCTGTCAGTACACTGGCCACATCAGTGGACACT 360
DB 407 GCCATGCTCAAGTTACAAAAGTCTCTGTCAGTACACTGGCCACATCAGTGGACACT 466
QY 361 CCAGCCCATCTTTAAAGCTACTGTGAGATCATGCTACCCACTTTCCTTTGATGAACAG 420
DB 467 CTTGCCATCTTTAAAGCTACTGTGAGATCATGCTACCCACTTTCCTTTGATGAACAG 526
QY 421 AACTGCAGCATGAGCTGGCCACTGACCTACGACCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 527 AACTGCAGCATGAGCTGGCCACTGACCTACGACCTGCTGCTGCTGCTGCTGCTGCTG 586
QY 481 GAAAGCCAGCAGCAGACCTGAGCACTTCATGGAGAGCGGGAGTGGGTGATCAAGGAG 540
DB 587 GAAAGCCAGCAGCAGACCTGAGCACTTCATGGAGAGCGGGAGTGGGTGATCAAGGAG 646
QY 541 TCCGGGGCTGGAGCACTCGTGGACCTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 647 TCGGGGGCTGGAGCACTCGTGGTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 706
QY 601 ATACCTTACCACCTTCGTCATGCGCGCTG 630
DB 707 ATACCTTACCACCTTCGTCATGCGCGCTG 736
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RESULT 3

AAV72829

ID AAV72829 standard; DNA; 705 BP.

XX

AC AAV72829;

XX

19-FEB-1999 (first entry)

XX

Human acetylcholine receptor alpha-subunit variant 1 encoding DNA.

DE

XX

KW Human; acetylcholine receptor alpha-subunit; hAChR; variant;

KW myasthenia gravis; autoimmune response; neuromuscular disorder;

KW diagnosis; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX WO9850544-A1.

XX

XX 12-NOV-1998.

XX

XX 06-MAY-1998; 98WO-1100211.

XX

XX 07-MAY-1997; 97IL-0120792.

XX

XX (YEDA) YEDA RES & DEV CO LTD.

XX

XX Barchan D, Fuchs S, Souroujon MC;

XX

XX WPI; 1998-610383/51.

XX

XX P-PSDB; AAW83381.

XX

XX Poly(peptide(s) modulating auto:immune response to acetyl:choline

XX receptor - comprise all or part of extracellular domain of human

XX acetyl:choline receptor alpha-sub:unit, useful in treatment and

XX diagnosis of myasthenia gravis

XX

XX Claim 91; Fig -; 58pp; English.

XX

XX The present sequence encodes a human acetylcholine receptor (hAChR)

XX alpha-subunit variant which is used as all or part of a protein for

XX CC modulating the autoimmune response of an individual to hAChR. The

XX protein can be administered to alleviate and/or treat myasthenia gravis

XX

XX

XX

XX

XX

CC (MG), and is useful for diagnosing the condition. It can be combined
CC with a suitable carrier in pharmaceutical compositions, and is useful
CC for such therapeutic (especially nasal or oral) administration and
CC diagnosis. MG is a human neuromuscular disorder, in which autoantibodies
CC against AChR bind to the receptor and interfere with signal transmission
CC from nerve to muscle at the neuromuscular junction. The extracellular
CC domain of the AChR alpha-subunit appears to be the prime target for
CC these autoantibodies, particularly the main immunogenic region (MIR).
CC The protein enables antigen-specific immunotherapy which suppresses only
CC adverse autoimmune responses whilst leaving overall immune system
CC intact, unlike current methods of treating MG using immunosuppressive
CC drugs e.g. steroids.
CC N.B. The present sequence is not given in the specification but has been
CC created by the indexer as specified in the claim using the sequences
CC given in the figures.

XX Sequence 705 BP; 177 A; 192 C; 181 G; 155 T; 0 other;

Query Match 86.58; Score 545; DB 19; Length 705;

Best Local Similarity 89.48; Pred. No. 1.7e-137;

Matches 630; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

QY 1 TCCGAACATGAGACCCGCTCTGGTGGCAAGCTATTAAAGACTACAGCAGCGTGGTGGG 60

DB 1 TCCGAACATGAGACCCGCTCTGGTGGCAAGCTATTAAAGACTACAGCAGCGTGGTGGG 60

QY 61 CCAGTGAAGACACCCGCGAGGTGCTGAGGTGTCACCGTGGCGCTGCAGCTGATACAGCTC 120

DB 61 CCAGTGAAGACACCCGCGAGGTGCTGAGGTGTCACCGTGGCGCTGCAGCTGATACAGCTC 120

QY 121 ATCAATGTGATGAAGTAAATCAGATCGTGACACCAATGTGGCTGTGAAC----- 172

DB 121 ATCAATGTGATGAAGTAAATCAGATCGTGACACCAATGTGGCTGTGAAC----- 172

QY 173 ----- 172

DB 173 ----- 172

QY 181 ATGCTAGATGTCACGCGCCGAGTGGCTGACTTTGGGAGTTCCTTTGTTCTCATCTG 240

QY 173 -----AGCAATGGTGGATTACAACTAAATGGAATCCAGATGACTATGGGGTGTG 225

DB 241 CAGGATGAGCAATGGTGGATTACAACTAAATGGAATCCAGATGACTATGGGGTGTG 300

QY 226 AAAAAAATTCACATTCCTTCAGAAAAGATCTGGGCGCCAGACCTTGTCTCTATAACGAT 285

DB 301 AAAAAAATTCACATTCCTTCAGAAAAGATCTGGGCGCCAGACCTTGTCTCTATAACGAT 360

QY 286 GCAGATGCTGACTTTGCTATTGTCACAAAGTTCACAAAGTTCCTGCGAGTACACTGGCCAC 345

DB 361 GCAGATGCTGACTTTGCTATTGTCACAAAGTTCACAAAGTTCCTGCGAGTACACTGGCCAC 420

QY 346 ATCACTGGGACACCTCCAGCCATCTTTAAAGTACTGTGAGATCATCGTCACCCACTTT 405

DB 421 ATCACTGGGACACCTCCAGCCATCTTTAAAGTACTGTGAGATCATCGTCACCCACTTT 480

QY 406 CCCTTTGATGAACAGAACTGAGCATGAAGCTGGGCGCTGGAGCCTAGGAGCGCTCTGTC 465

DB 481 CCCTTTGATGAACAGAACTGAGCATGAAGCTGGGCGCTGGAGCCTAGGAGCGCTCTGTC 540

QY 466 GTGGCCATCAACCGGAAAGCGACCCAGACCTGAGCACTTCATGAGAGCGGGGAG 525

DB 541 GTGGCCATCAACCGGAAAGCGACCCAGACCTGAGCACTTCATGAGAGCGGGGAG 600

QY 526 TGGGTGATCAAGAGTCCCGGGCTGGAAGCAGTCCGCTGACCTATTCTGCTGCCCGAC 585

DB 601 TGGGTGATCAAGAGTCCCGGGCTGGAAGCAGTCCGCTGACCTATTCTGCTGCCCGAC 660

QY 586 ACCCCCTACCTGGACATCACTACCTACCTACCTACCTACCTACCTACCTACCTACCT 630

DB 661 ACCCCCTACCTGGACATCACTACCTACCTACCTACCTACCTACCTACCTACCTACCT 705

RESULT 4

AAV72830

ID AAV72830 standard; DNA; 690 BP.
 AC AAV72830;
 XX
 XX 19-FEB-1999 (first entry)
 XX
 XX Human acetylcholine receptor alpha-subunit variant 2 encoding DNA.
 XX
 XX Human; acetylcholine receptor alpha-subunit; hAChR; variant;
 KW myasthenia gravis; autoimmune response; neuromuscular disorder;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO9850544-A1.
 XX
 XX 12-NOV-1998.
 PD
 XX
 XX 06-MAY-1998; 98WO-IL00211.
 PF
 XX 07-MAY-1997; 97IL-0120792.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Barchan D, Fuchs S, Souroujon MC;
 XX
 XX WPI; 1998-610383/51.
 DR P-PSDB; AAW83382.
 XX
 XX
 PT Poly:peptide(s) modulating auto:immune response to acetyl:choline
 receptor - comprise all or part of extracellular domain of human
 PT acetyl:choline receptor alpha-sub:unit, useful in treatment and
 PT diagnosis of myasthenia gravis
 XX
 PS Claim 9ii; Fig -: 58pp; English.
 XX
 CC The present sequence encodes a human acetylcholine receptor (hAChR)
 CC alpha-subunit variant which is used as all or part of a protein for
 CC modulating the autoimmune response of an individual to hAChR. The
 CC protein can be administered to alleviate and/or treat myasthenia gravis
 CC (MG), and is useful for diagnosing the condition. It can be combined
 CC with a suitable carrier in pharmaceutical compositions, and is useful
 CC for such therapeutic (especially nasal or oral) administration and
 CC diagnosis. MG is a human neuromuscular disorder, in which autoantibodies
 CC against AChR bind to the receptor and interfere with signal transmission
 CC from nerve to muscle at the neuromuscular junction. The extracellular
 CC domain of the AChR alpha-subunit appears to be the prime target for
 CC these autoantibodies, particularly the main immunogenic region (MIR).
 CC The protein enables antigen-specific immunotherapy which suppresses only
 CC adverse autoimmune responses whilst leaving overall immune system
 CC intact, unlike current methods of treating MG using immunosuppressive
 CC drugs e.g. steroids.
 CC N.B. The present sequence is not given in the specification but has been
 CC created by the indexer as specified in the claim using the sequences
 CC given in the figures.
 XX
 SQ Sequence 690 BP; 175 A; 187 C; 176 G; 152 T; 0 other;

Query Match 84.1%; Score 530; DB 19; Length 690;
 Best Local Similarity 89.1%; Pred. No. 1.9e-133;
 Matches 615; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

QY 1 TCCGAACATGAGACCGCTCTGGTGCACAAAGCTATTAAAGACTACAGCAGCGTGGTGGG 60
 DB 1 TCCGAACATGAGACCGCTCTGGTGCACAAAGCTATTAAAGACTACAGCAGCGTGGTGGG 60
 QY 61 CCAGTGGGAAGACACCGCCAGCGTCTGGAGTGCACCGTGGCGCTGCAGCTGATACAGTCT 120
 DB 61 CCAGTGGGAAGACACCGCCAGCGTCTGGAGTGCACCGTGGCGCTGCAGCTGATACAGTCT 120
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 DB 121 ATCAATGTGGATGAAGTAAATCAGATCTGACACCAATGTGCGTCTGAAACAGGGTGAC 180
 QY 173 -----
 DB 181 ATGGTAGATCTGCCACGCCCGAGCTGCGTACTTTGGGAGTTCCCTTTCTTCATCTG 240
 QY 173 -----AGCAATGGGTGGATTACAACTAAATGGAATCCAGATGACTATGGCGGTGG 225
 DB 241 CAGGATGAGCAATGGGTGGATTACAACTAAATGGAATCCAGATGACTATGGCGGTGG 300
 QY 226 AAAAAAATTCACATTCCTTCAGAAAAGATCTGGCCGCCAGACCTTGTCTCTATAACGAT 285
 DB 301 AAAAAAATTCACATTCCTTCAGAAAAGATCTGGCCGCCAGACCTTGTCTCTATAACGAT 360
 QY 286 GCAGATGTGACTTTGTCTATTGTCAAGTTACCAAAAGTCTCCTGCAGTACACTGGCCAC 345
 DB 361 GCAGATGTGACTTTGTCTATTGTCAAGTTACCAAAAGTCTCCTGCAGTACACTGGCCAC 420
 QY 346 ATCAGTGGACACCTCCAGCCATCTTTAAAGCTACTGTGAGATCATCGTCACCCACTTT 405
 DB 421 ATCAGTGGACACCTCCAGCCATCTTTAAAGCTACTGTGAGATCATCGTCACCCACTTT 480
 QY 406 CCTTTGATGACAGAACTGCAGCATGAAGCTGGGCACCTGGACCTAGACGGCTCTGTC 465
 DB 481 CCTTTGATGACAGAACTGCAGCATGAAGCTGGGCACCTGGACCTAGACGGCTCTGTC 540
 QY 466 GTGGCCATCAACCCGGAAGCGACCCAGCAGACCTGAGCAACTTCATGGAGCGGGAG 525
 DB 541 GTGGCCATCAACCCGGAAGCGACCCAGCAGACCTGAGCAACTTCATGGAGCGGGAG 600
 QY 526 TGGGTGATCAAGGAGTCCCGGGGCTGGAAGCAGCTCCGTGACCTATTCCTGCTGCCCGAC 585
 DB 601 TGGGTGATCAAGGAGTCCCGGGGCTGGAAGCAGCTCCGTGACCTATTCCTGCTGCCCGAC 660
 QY 586 ACCCCCTACTTGGACATCACTACCATTC 615
 DB 661 ACCCCCTACTTGGACATCACTACCATTC 690

RESULT 5
 AAV72831
 ID AAV72831 standard; DNA; 363 BP.
 XX
 AC AAV72831;
 XX
 XX 19-FEB-1999 (first entry)
 DT
 XX Human acetylcholine receptor alpha-subunit variant 3 encoding DNA.
 DE
 XX Human; acetylcholine receptor alpha-subunit; hAChR; variant;
 KW myasthenia gravis; autoimmune response; neuromuscular disorder;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO9850544-A1.
 XX
 XX 12-NOV-1998.
 PD
 XX 06-MAY-1998; 98WO-IL00211.
 PF
 XX 07-MAY-1997; 97IL-0120792.
 PR
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Barchan D, Fuchs S, Souroujon MC;
 XX
 XX WPI; 1998-610383/51.
 DR P-PSDB; AAW83383.
 XX
 XX Poly:peptide(s) modulating auto:immune response to acetyl:choline
 PT receptor - comprise all or part of extracellular domain of human


```
Db 97 CAGUGGAGCAUACACCCACCUUUGAGUAUACAGUGGGCCUACAGCUGUAUACAACUC 156
Qy 121 AFCAATGTGGATGAAGTAATAGATCGTGACAAACCAATGTGCGTCTGAAACAGCAATGG 180
Db 157 AUCAGUGUGGAUAGUAUACAAUUGUGGAAACAAUUGUGCGGCCUAAAGCAGCAUUGG 216
Qy 181 GTGGATTACACCTTAAATGGATCCAGATGACTATGCGGTGCGGTGTAAGAAATTCACATT 240
Db 217 AUGAUGUGAGGCGUCGUGGAAUCCAGCGGAUUAUUGGUAUUAUAAAGAUCAAGACUG 276
Qy 241 CCGTTCAGAAAGATCTGCGGCCACGACCTGTCTCTATACGATGACAGATGGTGCATT 300
Db 277 CCUCUGAUGAUGUUGGCGCCAGUAUUGUUCUACAAUUGCUGAUGGUGUAUUU 336
Qy 301 GCTATTGTCAAGTTCCACAAAGTCTCTGTCAGTACATGCGCCACAT---CACGTGGACA 357
Db 337 GCGAUGUGUACAUAGACCAACACUGCUUUGGAUUAUACGGGAAUUAUUAUGUGGACA 396
Qy 358 CCGCAGCCATCTTTAAAGTCTAGATCATCGTACCCAGCTTTCCTTTGATGAA 417
Qy 397 CCUCAGCAUUCUCAAAGCAUUGGAAU---GUAACACAUUUCUCCAUUGAUCAA 453
Qy 418 CAGAACTCAGCATGAAGCTGGGACCTGGACCTACGACGCTCTGTCTGGCCATCAAC 477
Db 454 CAUAUUCACUAUGAAGUUGGAAUUGGAGUAGGACGAAUUAUUGUCCAUUCC 513
Qy 478 CCGGAAAGCGACCGACGCTGAGCAACTTCATGAGAGCGGGAGTGGGTGATCAAG 537
Db 514 CCGGAAAGUAGCCGCGGACUGAGUACUUAUUGGAAUUGGAGUGGUGGUAUAGAA 573
Qy 538 GAGTCCCGGGCTGGAAGCACTCGGTGACCTATTCCTGCTGCTCCCGGACACCCCTACCTG 597
Db 574 GAUAUUGUGAUGAAGCAUUGGUGUAUUAUACUGUGUUGUACUGUGUACUCCUACUG 633
Qy 598 GACATCACTACCACTTCGTCATGACGCG 626
Db 634 GAUAUCCUACCAUUAUUAUUGAUGGCG 662

RESULT 10
AAV72832
ID AAV72832 standard; DNA; 438 BP.
XX
AC AAV72832;
XX
DT 19-FEB-1999 (first entry)
XX

Human acetylcholine receptor alpha-subunit variant 4 encoding DNA.
Human; acetylcholine receptor alpha-subunit; hAChR; variant;
myasthenia gravis; autoimmune response; neuromuscular disorder;
diagnosis; ss.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN W09850544-A1.
XX
XX
PD 12-NOV-1998.
XX
XX
PF 06-MAY-1998; 98WO-IL00211.
XX
PR 07-MAY-1997; 97IL-0120792.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
XX
PI Barchan D, Fuchs S, Souroujon MC;
XX
XX WPI; 1998-610383/51.
DR
DR P-PSDB; AAW83384.
XX
PT Poly:peptide(s) modulating auto:immune response to acetyl:choline
```

```
receptor - comprise all or part of extracellular domain of human
acetyl:choline receptor alpha-sub:unit, useful in treatment and
diagnosis of myasthenia gravis
Claim 9iv; Fig -: 58pp; English.
The present sequence encodes a human acetylcholine receptor (hAChR)
alpha-subunit variant which is used as all or part of a protein for
modulating the autoimmune response of an individual to hAChR. The
protein can be administered to alleviate and/or treat myasthenia gravis
(MG), and is useful for diagnosing the condition. It can be combined
with a suitable carrier in pharmaceutical compositions, and is useful
for such therapeutic (especially nasal or oral) administration and
diagnosis. MG is a human neuromuscular disorder, in which autoantibodies
against AChR bind to the receptor and interfere with signal transmission
from nerve to muscle at the neuromuscular junction. The extracellular
domain of the AChR alpha-subunit appears to be the prime target for
these autoantibodies, particularly the main immunogenic region (MIR).
The protein enables antigen-specific immunotherapy which suppresses only
adverse autoimmune responses whilst leaving overall immune system
intact, unlike current methods of treating MG using immunosuppressive
drugs e.g. steroids.
N.B. The present sequence is not given in the specification but has been
created by the indexer as specified in the claim using the sequences
given in the figures.
SQ Sequence 438 BP; 116 A; 106 C; 113 G; 103 T; 0 other;
Query Match 44.1%; Score 278; DB 19; Length 438;
Best Local Similarity 82.9%; Pred. No. 2.4e-65;
Matches 363; Conservative 0; Mismatches 0; Indels 75; Gaps 1;
Qy 1 TCCGAACATGAGACCGCTCTGCTGTCGCAAGCTATTAAAGACTACAGCAGCGTGGTGGG 60
Db 1 TCCGAACATGAGACCGCTCTGCTGTCGCAAGCTATTAAAGACTACAGCAGCGTGGTGGG 60
Qy 61 CCAGTGGAAAGACACCGCCAGGTCTGAGAGTCAACCGTGGCCCTGCAGCTGATACAGCTC 120
Db 61 CCAGTGGAAAGACACCGCCAGGTCTGAGAGTCAACCGTGGCCCTGCAGCTGATACAGCTC 120
Qy 121 ATCAATGTGGATGAAGTAATACAGATCGTGACACCAATGTGCGTCTGAAACAGCGTGC 172
Db 121 ATCAATGTGGATGAAGTAATACAGATCGTGACACCAATGTGCGTCTGAAACAGCGTGC 180
Qy 173 ----- 172
Db 181 ATGTAGATCTGCCACGCCCGCAGCTGGGTGACTTTGGAGTTCCTTTTCTCATCTG 240
Qy 173 -----AGCAATGGTGGATTACAACTAAATGGGAATCCAGATGACTATGGCGGTGTG 225
Db 241 CAGGATGAGCAATGGTGGATTACAACTAAATGGGAATCCAGATGACTATGGCGGTGTG 300
Qy 226 AAAAAATTCACATTCCTTCAGAAAGATCTGGCGCCAGACCTTGTCTCTATAACGAT 285
Db 301 AAAAAATTCACATTCCTTCAGAAAGATCTGGCGCCAGACCTTGTCTCTATAACGAT 360
Qy 286 GCAGATGGTGAATTTGCTATTGTCAAGTTCACCAAAAGTCTCTGCGAGTACACTGGCCAC 345
Db 361 GCAGATGGTGAATTTGCTATTGTCAAGTTCACCAAAAGTCTCTGCGAGTACACTGGCCAC 420
Qy 346 ATCAGTGGACACCTCCA 363
Db 421 ATCAGTGGACACCTCCA 438

RESULT 11
AAV72833
ID AAV72833 standard; DNA; 267 BP.
XX
AC AAV72833;
XX
DT 19-FEB-1999 (first entry)
XX
```

DE Human acetylcholine receptor alpha-subunit variant 5 encoding DNA.
XX
KW Human; acetylcholine receptor alpha-subunit; hAChR; variant;
KW myasthenia gravis; autoimmune response; neuromuscular disorder;
diagnosis; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO980544-A1.
XX
PD 12-NOV-1998.
XX
PF 06-MAY-1998; 98WO-IL00211.
XX
PR 07-MAY-1997; 97IL-0120792.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX Barchan D, Fuchs S, Souroujon MC;
DR WPI; 1998-610383/51.
DR P-PSDB; AAW83385.
XX
XX Poly:peptide(s) modulating auto:immune response to acetyl:choline
receptor - comprise all or part of extracellular domain of human
acetyl:choline receptor alpha-sub:unit, useful in treatment and
diagnosis of myasthenia gravis
XX
PS Claim 9v; Fig -; 58pp; English.
XX
CC The present sequence encodes a human acetylcholine receptor (hAChR)
alpha-subunit variant which is used as all or part of a protein for
modulating the autoimmune response of an individual to hAChR. The
protein can be administered to alleviate and/or treat myasthenia gravis
(MG), and is useful for diagnosing the condition. It can be combined
with a suitable carrier in pharmaceutical compositions, and is useful
for such therapeutic (especially nasal or oral) administration and
diagnosis. MG is a human neuromuscular disorder, in which autoantibodies
against AChR bind to the receptor and interfere with signal transmission
from nerve to muscle at the neuromuscular junction. The extracellular
domain of the AChR alpha-subunit appears to be the prime target for
these autoantibodies, particularly the main immunogenic region (MIR).
The protein enables antigen-specific immunotherapy which suppresses only
adverse autoimmune responses whilst leaving overall immune system
intact, unlike current methods of treating MG using immunosuppressive
drugs e.g. steroids.
XX
XX N.B. The present sequence is not given in the specification but has been
created by the indexer as specified in the claim using the sequences
given in the figures.
XX
SQ Sequence 267 BP; 61 A; 86 C; 68 G; 52 T; 0 other;
Query Match 42.4%; Score 267; DB 19; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.9e-62;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 364 GCCATCTTTAAAGTACTGTGAGATCATGTCACCCATTTCCCTTTTCATGACAGAAC 423
DB 1 GCCATCTTTAAAGTACTGTGAGATCATGTCACCCATTTCCCTTTTCATGACAGAAC 60
QY 424 TGCAGATGAAGCTGGGACCTGGACCTACGAGCGCTCTGTCTGGCCCATCAACCCGGAA 483
DB 61 TGCAGATGAAGCTGGGACCTGGACCTACGAGCGCTCTGTCTGGCCCATCAACCCGGAA 120
QY 484 ACGGACCCAGACCTGAGCAACTTCATGGAGAGGGGGAGTGGTGATCAAGGATCC 543
DB 121 ACGGACCCAGACCTGAGCAACTTCATGGAGAGGGGGAGTGGTGATCAAGGATCC 180
QY 544 CGGGGCTGGAAGCACTCCGTGACCTATTCTGCTGCCCGACACCCCTACCTGGACATC 603
DB 181 CGGGGCTGGAAGCACTCCGTGACCTATTCTGCTGCCCGACACCCCTACCTGGACATC 240

QY 604 ACCTACCACTTCGTATGTCAGCGCCTG 630
DB 241 ACCTACCACTTCGTATGTCAGCGCCTG 267
RESULT 12
AAV12199
ID AAV12199 standard; cDNA; 2277 BP.
XX
AC AAV12199;
XX
DT 14-MAY-1998 (first entry)
XX
DE Human neuronal nicotinic acetylcholine receptor alpha-2 subunit cDNA.
XX
KW Human; neuronal nicotinic acetylcholine receptor; alpha-2 subunit;
KW brain tissue; screening; NACHR; antibody; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 166..1755
CDS /*tag= a
FT /*product= "neuronal nicotinic acetylcholine receptor
alpha-2 subunit"
XX
PN WO9420617-A2.
XX
PD 15-SEP-1994.
XX
PF 08-MAR-1994; 94WO-US02447.
XX
PR 08-MAR-1993; 93US-0028031.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI Elliott KJ, Ellis SB, Harpold MM;
XX WPI; 1994-303024/37.
XX P-PSDB; AAW44155.
XX
PT Human neuronal nicotinic acetylcholine receptor subunits and DNA -
PT also transformed cells useful for screening cpds. which modulate
PT activity of the receptor
XX
PS Disclosure; Page 67-68; 99pp; English.
XX
CC The present sequence encodes a human neuronal nicotinic acetylcholine
receptor (NACHR) subunit. The cells expressing the alpha and/or beta
NACHR subunits may be used in a method of screening compounds to
identify any which modulate the activity of human neuronal NACHR.
CC Subunit specific antibodies may be used to monitor the distribution
and expression density of various subunits in normal vs diseased brain
tissues. Testing of single receptor subunits or specific receptor
CC subunit combinations with a variety of potential agonists or antagonists
provides information with respect to the function and activity of the
individual subunits and should lead to the identification and design of
CC compounds that are capable of very specific interaction with one or
more receptor subtypes. The resulting drugs should exhibit fewer
CC unwanted side effects than drugs identified e.g. screening with cells
XX that express a variety of subtypes.
SQ Sequence 2277 BP; 451 A; 695 C; 643 G; 486 T; 2 other;
Query Match 35.6%; Score 224.2; DB 15; Length 2277;
Best Local Similarity 60.9%; Pred. No. 1.6e-50;
Matches 383; Conservative 0; Mismatches 243; Indels 3; Gaps 1;
QY 2 CCGACATGAGACCCCTCTGGTGGCAAGCTATTTAAAGACTACACGCGTGGCGGC 61
DB 332 CCGAGCTGAGGACCGGCTCTTAAACACCTCTTCCGGGGCTACAAACCGCTGGCGGC 391

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 15:11:07 ; Search time 2255 Seconds

(without alignments)
4524.681 Million cell updates/sec

Title: US-09-820-339A-1

Perfect score: 630

Sequence: 1 tcggaacatgagaccgtct.....acttcgtcatgcagcgctg 630

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	617.4	98.0	864	9	AU120692	AU120692 AU120692
2	548.2	87.0	837	13	BI114221	BI114221 602862588
3	519.6	82.5	713	12	BF309251	BF309251 601890196
4	505.2	80.2	806	12	BF305214	BF305214 601892667
5	499.6	79.3	660	12	BF307986	BF307986 601894231
6	463.4	73.6	651	10	BB613689	BB613689 BB613689

7	448.6	71.2	566	9	AA596914	AA596914 vo21f03.r
8	439.8	69.8	946	9	AA755688	AA755688 vu12f02.r
9	418.2	66.4	554	10	BE664308	BE664308 148713 MA
10	393.2	62.4	497	9	AA636794	AA636794 vr16d12.r
11	383.8	60.9	479	9	AA636687	AA636687 vr15f05.r
12	346.4	55.0	853	14	B0735223	B0735223 AGENCOURT
13	345.8	54.9	713	13	B064207	B064207 BJ064207
14	345.8	54.9	862	14	B0733592	B0733592 AGENCOURT
15	343.2	54.5	494	9	AA688563	AA688563 vu17b11.r
16	325.2	51.6	495	9	AA692456	AA692456 vt21e02.r
17	324.4	51.5	632	13	BJ035634	BJ035634 BJ035634
18	318.6	50.6	651	14	BQ523257	BQ523257 NISC_n121
19	314.6	49.9	606	13	BQ031137	BQ031137 BJ031137
20	313.4	49.7	682	12	BG018521	BG018521 daa46h12.
21	312.6	49.6	615	13	BJ032622	BJ032622 BJ032622
22	311.4	49.4	397	9	AA596126	AA596126 vol17e09.r
23	296.8	47.1	650	14	BQ520897	BQ520897 NISC_n107
24	276.8	43.9	542	13	BJ040974	BJ040974 BJ040974
25	266	42.2	531	13	BQ065441	BQ065441 BJ065441
26	266	42.2	642	13	BQ062932	BQ062932 BJ062932
27	261.6	41.5	953	12	BG828551	BG828551 602752696
28	249	39.5	608	14	BM729043	BM729043 UI-E-E01-
29	241.2	38.3	667	13	BQ069932	BQ069932 BJ069932
30	238.8	37.9	610	13	BQ075194	BQ075194 BJ075194
31	233.2	37.0	460	13	BQ041265	BQ041265 BJ041265
32	223	35.4	693	13	BQ068841	BQ068841 BJ068841
33	213.6	33.9	358	9	AA673472	AA673472 vn46h11.r
34	210.2	33.4	563	13	BI195946	BI195946 602756234
35	207.2	32.9	355	12	BE899992	BE899992 149491 MA
36	201.4	32.0	758	14	BQ442306	BQ442306 UI-N-EX0-
37	199.2	31.6	882	13	BI195149	BI195149 602944157
38	197	31.3	755	10	AW914206	AW914206 EST345510
39	195.4	31.0	537	10	AW787186	AW787186 120930 MA
40	191.2	30.3	694	13	BI194994	BI194994 602944249
41	188.2	29.9	358	12	BF827782	BF827782 CM4-HN002
42	186.2	29.6	669	10	BQ653265	BQ653265 BB653265
43	185.2	29.4	687	10	BB639700	BB639700 BB639700
44	184.4	29.3	891	9	AI110117	AI110117 GH09582.5
45	184	29.2	660	10	BB665088	BB665088 BB665088

ALIGNMENTS

RESULT 1
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LOCUS AU120692 HEMBB1 Homo sapiens cDNA clone HEMBB1001217 5', mRNA 864 bp linear EST 01-AUG-2002
DEFINITION AU120692 sequence.
ACCESSION AU120692
VERSION AU120692.1 GI:10935927
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 864)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

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FEATURES source Location/Qualifiers
1. .864
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HEMBB1001217"
/clone_lib="HEMBB1"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"
BASE COUNT 200 a 249 c 214 g 198 t 3 others
ORIGIN
Query Match 98.0%; Score 617.4; DB 9; Length 864;
Best Local Similarity 99.7%; Pred. No. 5e-158;
Matches 629; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 TCCGAACATGAGACCCGCTGCTGGCAAGCTATTTAAAGCTACAGCAGCGTGGTGGG 60
Db 81 TCCGAACATGAGACCCGCTGCTGGCAAGCTATTTAAAGCTACAGCAGCGTGGTGGG 140
61 CCAGTGAAGACACCCGCCAGGTCGTGGAGGTACCGGTGGGCTGCGAGTGATACAGCTC 120
141 CCAGTGAAGACACCCGCCAGGTCGTGGAGGTACCGGTGGGCTGCGAGTGATACAGCTC 200
121 ATCAATGTGATGAAGTAATAGATCGTGACACCAACATGTGGTCTGAAACAGCAATGG 180
201 ATCAATGTGATGAAGTAATAGATCGTGACACCAACATGTGGTCTGAAACAGCAATGG 260
181 GTGGATTACAACTTAAATGGAATCCAGATGACTATGCGCGGTGTG-AAAAAAATTCACAT 239
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300 TGCTATTGTCAAGTTCACCAAGTCTCTGCGAGTACATGCGCAGATCAGTGGACACC 359
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360 TCCAGCATCTTTAAAGCTACTGTGAGATCATCGTCACCCACTTTCCTTTCATGAACA 419
441 TCCAGCATCTTTAAAGCTACTGTGAGATCATCGTCACCCACTTTCCTTTCATGAACA 500
420 GAATGCGAGCATGAAGTGGGACCTGGACCTACGAGCGGCTCTGCTGGCCATCAACCC 479
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480 GGAAGCGACACCGACCTGAGCACTTCATGGAGAGCGGGAGTGGTGTATCAGGA 539
561 GGAAGCGACACCGACCTGAGCACTTCATGGAGAGCGGGAGTGGTGTATCAGGA 620
540 GTCCCGGGGTGGAAGCAGCTCCGCTGACCTATTCCTGCTGCGCCGACACCCCTACCTGGA 599
621 GTCCCGGGGTGGAAGCAGCTCCGCTGACCTATTCCTGCTGCGCCGACACCCCTACCTGGA 680
QY 600 CATCACTTACCACTTCGTCTATGAGCGGCGCTG 630
Db 681 CATCACTTACCACTTCGTCTATGAGCGGCGCTG 711
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LOCUS 602862588F1 NIH_MGC_17 Homo sapiens cdna clone IMAGE:5021829 5',
DEFINITION mRNA sequence.
ACCESSION Bill14221
VERSION Bill14221.1 GI:14565122
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

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REFERENCE 1 (bases 1 to 837)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: AFCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1840 row: p column: 22
High quality sequence stop: 696.
FEATURES
Location/Qualifiers
1. .837
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HEMBB1001217"
/clone_lib="HEMBB1"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site:1: EcoRI;
Site:2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 204 a 232 c 213 g 188 t

ORIGIN

Query Match 87.0%; Score 548.2; DB 13; Length 837;
Best Local Similarity 94.9%; Pred. No. 4.4e-139;
Matches 599; Conservative 0; Mismatches 28; Indels 4; Gaps 3;

QY 1 TCCGAACATGAGACCCGCTGCTGGCAAGCTATTTAAAGCTACAGCAGCGTGGTGGG 60
Db 121 TCCGAACATGAGACCCGCTGCTGGCAAGCTATTTAAAGCTACAGCAGCGTGGTGGG 180
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Db 181 CCAGTGAAGACACCCGCCAGGTCGTGGAGGTACCGGTGGGCTGCGAGTGATACAGCTC 240
QY 121 ATCAATGTGATGAAGTAATAGATCGTGACACCAACATGTGGTCTGAAACAGCAATGG 180
Db 241 ATCAATGTGATGAAGTAATAGATCGTGACACCAACATGTGGTCTGAAACAGCAATGG 300
QY 181 GTGGATTACAACTTAAATGGAATCCAGATGACTATGCGCGGTGTGAAAAAAATTCACATT 240
Db 301 GTGGATTACAACTTAAATGGAATCCAGATGACTATGCGCGGTGTGAAAAAAATTCACATT 360
QY 241 CCTTCAGAAAGATCTGGCGCCAGACCTTGTCTCTATATACGATGCGATGCGACTTT 300
Db 361 CCTTCAGAAAGATCTGGCGCCAGACCTTGTCTCTATATACGATGCGATGCGACTTT 420
QY 301 GCTATTGTCAAGTTCACCAAGTGTCTCTGAGTACACTGCCACATCAGTGGACACCT 360
Db 421 GCTATTGTCAAGTTCACCAAGTGTCTCTGAGTACACTGCCACATCAGTGGACACCT 480
QY 361 CCAGCCATCTTTAAAGCTACTGTGAGATCATGTCACCCACTTTTCCCTTTTGTGAACAG 420
Db 481 CCAGCCATCTTTAAAGCTACTGTGAGATCATGTCACCCACTTTTCCCTTTTGTGAACAG 540
QY 421 AACTGAGCATGAAGTGGGCACTTGGACCTTACGAGCGTCTGTCTGTTGGCCATCAACCCG 480
Db 541 AACTGAGCATGAAGTGGGCACTTGGACCTTACGAGCGTCTGTCTGTTGGCCATCAACCCG 600
QY 481 GAAAGCGACACCGACCTGAGCACTTTCATGAGAGCGGGAGTGGTGTATCAGGA 540
Db 601 GAAAGCGACACCGACCTGAGCACTTTCATGAGAGCGGGAGTGGTGTATCAGGA 658

[illegible]

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FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:4138360"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pORF7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCCAGCAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```


Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 485.

FEATURES

source

1. .566
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCGAATCTGAAGTGGAGCGCGCCCTTTTGTTCGATCTGTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."

BASE COUNT 155 a 140 c 149 g 122 t
ORIGIN

Query Match 71.2%; Score 448.6; DB 9; Length 566;
Best Local Similarity 89.2%; Pred. No. 6.5e-112;
Matches 495; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 1 TCGAATCATGAGCCGCTCG-TGGCAAGACTATTAAAGACTACAGAGCTGGTGGC 59
Db 8 TCGAATCATGAGCCGCTCGTGTGGCAAGACTTTTGAAGACTACAGAGCTAGTCCG 67
QY 60 GCCAGTGGAAAGACCCCGGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 119
Db 68 GCCAGTGGAGACCCCGGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 127
QY 120 CATCAATGTGGATGAAGTAATCAGATCGTGACAACTATGCGTGTGAACAGCAATG 179
Db 128 TATCAATGTGGATGAAGTAATCAGATCGTGACAACTATGCGTGTGAACAGCAATG 187
QY 180 GGTGGATTACAACTAAATGGATCCAGATGACTATGGCGGTGTGNAATAATTCACAT 239
Db 188 GGTGGATTACAACTAAATGGATCCAGATGACTATGGCGGTGTGNAATAATTCACAT 247
QY 240 TCCTTCAGAAAGATCGGCGCCAGACCTTGTCTCTATAACGATCAGATGGTACTT 299
Db 248 CCCTCGAANAAGATCGGCGCGGAGCTGCTTCCTATATAACGATCAGATGGTACTT 307
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Db 308 TGCAATTTCAATTCACCAAGTGTCTTCGAGTACACTGGCCACATCAGTGGACAC 367
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Db 428 GAATTCGAGCATGAAGTGGGACCTTGGACCTATGAGCGGTCTGTCTGGCCATCAACCC 487
QY 480 GGAAGCGACCGACCTGAGCAACTTCATGGAGAGCGGGAGTGGGTGATCAAGGA 539
Db 488 GGAAGCGACCGACCTGAGCAACTTCATGGAGAGCGGGAGTGGGTGATCAAGGA 547
QY 540 GTCCCGGGGTGGNA 554
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Db 548 AGCTCGGGGCTGGAA 562

RESULT 8

AA755688

LOCUS

DEFINITION

AA755688 946 bp mRNA linear EST 21-JAN-1998

vul2f02.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone

IMAGE:1180443 5' similar to gb:Y00762 ACETYLCHOLINE RECEPTOR

PROTEIN, ALPHA CHAIN PRECURSOR (HUMAN); gb:X03986 Mouse mRNA for

muscle nicotinic acetylcholine receptor (MOUSE); mRNA sequence.

AA755688

AA755688.1 GI:2802886

EST.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mamma 1 (bases 1 to 946)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:638291

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 508.

Location/Qualifiers

1. .946

/organism="Mus musculus"

/strain="C3H"

/db_xref="taxon:10090"

/clone_lib="Barstead mouse myotubes MPLRB5"

/cell_line="C2C12"

/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTCGAATCTGAAGTGGAGCGCGCCCTTTTGTTCGATCTGTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

[AATTCGGATCCTTG], digested with Not I and cloned into the

Not I and Eco RI sites of the modified pT7T3 vector.

Library constructed by Bob Barstead. The C2C12 cell line

(available from ATCC, catalog # CRL-1772) differentiates

rapidly, forming contractile myotubes and producing

characteristic muscle proteins."

BASE COUNT 231 a 248 c 242 g 224 t

ORIGIN

Query Match 69.8%; Score 439.8; DB 9; Length 946;

Best Local Similarity 85.4%; Pred. No. 2.2e-109;

Matches 537; Conservative 0; Mismatches 87; Indels 5; Gaps 4;

QY 1 TCGAATCATGAGCCGCTCG-TGGCAAGACTATTAAAGACTACAGAGCTGGTGGC 59

Db 69 TCGAATCATGAGCCGCTCGTGTGGCAAGACTTTTGAAGACTACAGAGCTAGTCCG 128

QY 60 GCCAGTGGAAAGACCCCGGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 119

Db 129 GCCAGTGGAGACCCCGGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 188

QY 120 CATCAATGTGGATGAAGTAATCAGATCGTGACAACTATGCGTGTGAACAGCAATG 179

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/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."
138 a 135 g 117 t
BASE COUNT
138 a 164 c

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Qy	301	GCTATTGTCAAGTTCACCAAGTGCTCCTCGAGTACACTGGCCACATACACTGGACACCT	360
Db	392	GCCATCGTCAAGTTCACCAAGTGCTCCTGGACATACACTGGCCACATACACTGGACACCT	451
Qy	361	CCAGCCATCTTTAAAAGCTACTGTGAGATCATCTGTCACCCACTTCCCTTTGATGAACAG	420
Db	452	CCTGCCATCTTTAAAAGCTACTGCGAGATCATCTGTCACCCACTTCCCTTTGACGAACAG	511

Db	452	CCTGCCATCTTTAAAGCTACTGGGAGATCATGTCACCCACTTTCCCTTTGACGAACAG	511
QY	421	AACTGCCAGCATGAAGCTGGGCACCTGGACCTTACGACGCGCTCTG	463
Db	512	AACTGCCAGCATGAAGCTGGGCACCTGGACCTATGATGGCTCG	554

RESULT 10	AA636794	497 bp	mRNA	linear	EST 22-Oct-1997
LOCUS	vr16d12.r1	Barstead mouse myotubes	MPLRB5	Mus musculus	cDNA clone
DEFINITION	IMAGE:1120823.5	similar to gb:M17640	Mouse	acetylcholine receptor	
		alpha-subunit	mRNA (MOUSE);	mRNA sequence.	

IMAGE:il20823.5 similar to gp.M1/040 Mouse acetylcholine receptor alpha-subunit mRNA (MOUSE);, mRNA sequence.

ACCESSION AA636794
VERSION AA636794.1 GI:2560573
KEYWORDS EST.

KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
	1 (bases 1 to 497)
REFERENCE	Marrs, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
AUTHORS	Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
	Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
	Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
	Waterston, R.

TITLE	JOURNAL	COMMENT
The WashU-HMI Mouse EST Project	Unpublished (1996)	Contact: Marra W/Mouse EST Project
WashU-HMI Mouse EST Project	Washington University School of Medicine	

WashU-HHMI Mouse EST Project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:610159

Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES

source
Location/Qualifiers
1. .497
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5]; TGTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTT 3'; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins." 1 others

BASE COUNT 137 a 123 c 127 g 109 t

ORIGIN

Query Match 62.4%; Score 393.2; DB 9; Length 497;

Best Local Similarity 88.8%; Pred. No. 8.9e-97;

Matches 436; Conservative 0; Mismatches 54; Indels 1; Gaps 1;

QY 40 GACTACAGCAGCGGTGGCGCCAGTGGAGACACCGCAGGTCTGGAGGTACCGTG 99
|||||
Db 8 GACTACAGCAGTGTAGT-TGGCCAGTGGAGACACCGTGAGATGTGACAGTACCGTG 66
QY 100 GGCCTGCAGCTGATACAGCTCATCAATGTGGATGAAGTAAATCAAGTCTGTCGACAAACCAAT 159
|||||
Db 67 GGTCTACAGCTGATCCAGCTTATCAATGTGGATGAAGTAAATCAAGTCTGTCGACAAACCAAT 126
QY 160 GTGGCTGTGAACAGCAATGGTGGATTACAACTAAATGGATCCAGATGATATGGC 219
|||||
Db 127 GTAGCTGTGAACAGCAATGGTGGATTACAACTTGAATGGAATCCAGAGCTATGGA 186
QY 220 GGTGTGAAAAAATTCACATTCCTTCAGAAAAGATCTGGCGCCCGCAGACCTTGTTCTCTAT 279
|||||
187 GGAGTGAATAAATTCACATCCCTCGGAAAAGATCTGGCGCCCGCAGCTCGTTCTCTAT 246
QY 280 AACGATGCAGATGGTGACTTGTCTATTGTCAAGTTCAACAAAGTCTCCTGCAGTACACT 339
|||||
Db 247 AACAAACGACGCGGACTTGGCAATGTCAATTCACCAAGGTGCTCTGGAGTACACC 306
QY 340 GGCCATCATCGTGGACACCTCCAGCCATCTTTAAAGTACTGTGAGATCATGTCACC 399
|||||
Db 307 GGCCATCATCGTGGACACCGCCAGCCATCTTTAAAGTACTGTGAGATCATGTCACT 366
QY 400 CACTTTCCCTTTGATGAACAGCACTGCAGCATGAGCTGGCCACCTGGACCTACGACGGC 459
|||||
Db 367 CACTTTCCCTTCGATGAGCAGAACTGCAGCATGAAGCTGGCCACCTGGACCTATGACGGC 426
QY 460 TCTGCTGCGCATCAACCCGGAAGGAGCAGCCAGCATCTGAGCAACTTCATGGAGAGC 519
|||||
Db 427 TCTGCTGNGCATTAACCCGGAAGGTGACACGCCCGACCTGAGTAACTTCATGGAGAGC 486
QY 520 GGGAGTGGGT 530
|||||
Db 487 GGGAGTGGGT 497

RESULT 11

AA636687

LOCUS

DEFINITION

vr15f05.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1120737 5', similar to gb:M17640 Mouse acetylcholine receptor alpha-subunit mRNA (MOUSE);, mRNA sequence.

AA636687

VERSION 1 GI:2560466

SOURCE EST.

ORGANISM house musculus

REFERENCE

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

TITLE

JOURNAL

COMMENT

Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 341.
MGI:610073
Location/Qualifiers
1. .479
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5]; TGTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTT 3'; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins." 1 others

FEATURES

source

BASE COUNT 130 a 118 c 124 g 106 t
ORIGIN

Query Match 60.9%; Score 383.8; DB 9; Length 479;
Best Local Similarity 88.8%; Pred. No. 3.3e-94;
Matches 426; Conservative 0; Mismatches 53; Indels 1; Gaps 1;
QY 100 GGCTGCAGCTGATACAGCTCATCAATGTGGATGAAGTAAATCAAGTCTGTCGACAAACCAAT 159
|||||
Db 1 GGCTGCAGCTGATACAGCTCATCAATGTGGATGAAGTAAATCAAGTCTGTCGACAAACCAAT 60
QY 160 GTGGCTGTGAACAGCAATGGTGGATTACAACTAAATGGATCCAGATGATATGGC 219
|||||
Db 61 GTAGCTGTGAACAGCAATGGTGGATTACAACTTGAATGGAATCCAGATGATATGGA 120
QY 220 GGCTGTGAATAAATTCACATTCCTTCAGAAAAGATCTGGCGCCCGCAGACCTTGTTCTCTAT 279
|||||
Db 121 GGAGTGAATAAATTCACATCCCTCGGAAAAGATCTGGCGCCCGCAGCTGTTCTCTAT 180
QY 280 AACGATGCAGATGGTGACTTGTCTATTGTCAAGTTCAACAAAGTCTCCTGCAGTACACT 339
|||||

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Db 181 AACACGACGAGCGGACTTTGCCATTGTCAAATTCACCAAGGTGCTCCTGGACTACACC 240
Qy 340 GGCACATCAGTGGACACCTCCAGCCATCTTTAAAGCTACTGTGAGATCATCTGTCACC 399
Db 241 GGCACATCAGTGGACACCTCCAGCCATCTTTAAAGCTACTGTGAGATCATCTGTCACC 300
Qy 400 CACTTCCCTTTGATGACAGCACTGACGATGAGCTGGCGGCTGACCTGACCTACGACGC 459
Db 301 CACTTCCCTTTGATGACAGCACTGACGATGAGCTGGCGGCTGACCTGACCTATGACGC 360
Qy 460 TCTGCTGGGCTCAACCCGAAAGCCAGCCAGCAGCACTGAGCACTTCATGGAGAGC 519
Db 361 TCTGCTGGGCTCAACCCGAAAGCCAGCAGCAGCAGCTGAGTACTTCATGGAGAGC 420
Qy 520 GGGGAGTGGGTATCAAGAGTCCCGGGCTGGAGCACTCCGAGCACTATTCCTGCTGC 579
Db 421 GGGGAGTGGGTATCAAGAGTCCCGGGCTGG-ATCACTGGGTGTTCTACTCCTGCTGC 479

JULY 12
LOCUS
DEFINITION AGENCOURT_8097435 NICHG XGC Emb4 Xenopus laevis cDNA clone EST 16-JUL-2002
IMAGE:5542583 5', mRNA sequence.
ACCESSION B0735223
VERSION B0735223
KEYWORDS EST.
SOURCE B0735223.1 GI:21874120
ORGANISM African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 853)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Plate: LLAM12242 row: b column: 24
High quality sequence stop: 647.
Location/Qualifiers
1..853
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5542583"
/clone.lib="NICHG XGC Emb4"
/dev_stage="embryo, stage 31-32"
/lab_host="DH10B (phage-resistant)"
Note: "Organ: whole embryo; Vector: pCMV-SPORT6; Site:1:
Noti; Site:2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."
BASE COUNT 229 a 169 c 188 g 266 t 1 others
ORIGIN

Query Match 55.0%; Score 346.4; DB 14; Length 853;
Best Local Similarity 71.9%; Pred. No. 7.9e-84;
Matches 452; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 1 TCCGAACATGAGACCCGCTGCTGGTGCACAGCTATTAAAGACTACAGCGGTGGTGGCG 60
Db 80 TCTGAGGATGAATCCCGCTTATATAATGACTATTCAAGAGCTACACAAAGTGTCTCT 139
Qy 61 CCATGGGAAGACCCCGGCTGCTGGAGGTGTCACCGTGGGCTGCAGCTGATACAGTCT 120

```

```

Db 140 CAGGTCAGGCTTTTAAAGACAAAGTTGTTGGTGACGGTGGGACTCCAGCTTTATACAGCTT 199
Qy 121 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCTGTGAACAGCAATGG 180
Db 200 ATTAATGTGAATGAAGTCAATCAATTTGTAAACAACAAATGTCTGCTGAACAGCAATGG 259
Qy 181 GTGGATTAACAACCTTAAATGGAATCCAGATGACTATGCGGGTGTGAACAAATTCACATT 240
Db 260 GAGGATGTTCACCTAAAGTGGGATCCAGAAGATTTTAAAGTATGAGGATCAAGAAAGTTCGATC 319
Qy 241 CTTTCAAGAAAGATGCGGGCCAGACCTTTCTCTATAACGATGCAGATGGTACATT 300
Db 320 CTTTCTAGTGATTTTGGCGCCTTGATATGTGCTGTAACAACATGCAGATGGAGACTTT 379
Qy 301 GCTATTGTCAAGTTTCAACAAAGTCTCTGACAGTACACATGCGCACATCAGTGGACACCT 360
Db 380 GCTATTGTCCAGAAACAAAGGCTCTCTGAGTACACATGCGGGAATAATATGTTGCTGCC 439
Qy 361 CCAGCATCTTTAAAGTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAG 420
Db 440 CTTGCAATTTTAAAGTACTGTGAAATGATTTGACATACATTTCCATTTGACCTACAG 499
Qy 421 RACTGCAGCATCAAGCTGGGACCTGGACCTAGCAGGGCTCTGTGCTGCCCATCAACCG 480
Db 500 AACTGCAGCATCAAGCTGGTACTGCGGACCTTACGATGGCACATTAGTTGTTATAATCCA 559
Qy 481 GAAAGCGACGACCTGAGCAACTTCATGGAGCGGGAGTGGGTGATCAAGGAG 540
Db 560 GAAATGATCGTCCAGATCTGAGTAACTTATGGAAGTGGAGATGGTACATGAAGAT 619
Qy 541 TCCCGGGGTGGAAGACATCCGTGACCTATTCCTGCTGCCCGACACCCCTACCTGGAC 600
Db 620 TATCGCTGCTGGAAGCACTGNGTTTATATGACTGCTGCCAGAACACCATCTTGGAT 679
Qy 601 ATCATTACCACTTCTGTCATGCGAGCGCT 629
Db 680 ATCATACTACCACTTTCTCTCGCAGAGGCT 708

RESULT 13
LOCUS B0735223 713 bp mRNA linear EST 07-DEC-2001
DEFINITION B0735223 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL078109 5', mRNA sequence.
ACCESSION B0735223
VERSION B0735223
KEYWORDS EST.
SOURCE B0735223.1 GI:17425045
ORGANISM African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 713)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..713
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL078109"
/clone.lib="NIBB Mochii normalized Xenopus tailbud
library"
/tissue_type="whole embryo"
FEATURES
source

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[illegible]

Search completed: January 14, 2003, 16:48:24
Job time : 2262 secs

BASE COUNT	127 a	133 c	120 g	114 t	ORIGIN
Query Match	54.5%	Score 343.2;	DB 9;	Length 494;	
Best Local Similarity	88.6%;	Pred. No. 4.4e-83;			
Matches 372;	Conservative 0;	Mismatches 48;	Indels 0;	Gaps 0;	
OY	1	TCGGAACATGAGACCGCGTCTGGTGGCAAGCTATTTAAAGACTACAGCAGCGTGGTGGCGG	60		
Ddb	75	TCGGAACATGAGACCGGCTGGTGGCAAGCTCTTTGAAGACTACAGCAGTGTAGTCCGG	134		
OY	61	CCAGTGGGAAGACACCGCCAGGTCGTGGAGGTCACCGTGGCGCTCGAGCTGATACAGCTC	120		
Ddb	135	CCAGTGGGAGGACACCGGTGAGATTGTACAACTCACCGTGGGTCTACAGCTGATCCAGCTT	194		

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1139	99.7	457	6	AAP50361		Human acetyl cholin
2	1139	99.7	457	21	AAV56386		Human acetylcholin
3	1133	99.1	437	22	AAU69151		Human Acetylcholin
4	1111.5	97.2	235	19	AAW83381		Human acetylcholin
5	1100.5	96.3	11	AAAR6254		Human acetylcholin	
6	1088.5	95.2	230	19	AAW83382		Human acetylcholin
7	1086.5	95.1	458	11	AAAR6256		Human acetylcholin
8	1074.5	94.0	456	11	AAAR6255		Calf acetylcholine
9	969.5	84.8	455	11	AAAR6257		Mouse acetylcholin
10	910	79.6	449	14	AAAR6258		Chicken acetylchol
10	910	79.6	449	14	AAAR6258		Acetylcholine rece

ET	/label= Eptope
ET	/note= "Claim 1 (VI

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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FT Active-site 407..412
FT /label= Epitope
FT /note= "Claim 1 (VII)"
XX
XX JP60078996-A.
XX
XX PD 04-MAY-1985.
XX
XX PF 05-OCT-1983; 83JP-0186402.
XX
XX PR 05-OCT-1983; 83JP-0186402.
XX
XX PA (MITU ) MITSUBISHI CHEM IND KK.
XX
XX WPI; 1985-144120/24.
XX
XX DR N-PSDB; AAN50415.
XX
XX PT New peptide(s) useful in treatment of myasthenia gravis - also in
XX diagnosis, having acetylcholine receptor-alpha like activities.
XX
XX PS Disclosure; Fig 1; 13pp; Japanese.
XX
XX CC Peptides derived from the hAChR-alpha gene product have similar
XX immunogenicity to the gene product, and may be useful in the
XX treatment and diagnosis of myasthenia gravis caused by neuropathy in
XX autoimmune reaction to AChR.
XX
XX SQ Sequence 457 AA;

Query Match 99.7%; Score 1139; DB 6; Length 457;
Best Local Similarity 99.5%; Pred. No. 2.3e-110;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDVNOQIVTTNVRKQOW 60
DB 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDVNOQIVTTNVRKQOW 80
QY 61 VDYNLKWNPDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIYKFTKVLQYTGHTWTP 120
DB 61 VDYNLKWNPDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIYKFTKVLQYTGHTWTP 140
QY 121 PAIFKYSCEIIVTHFFPDEQNSMKLGTTWTYDGSVVAINPESQDPDLNFMESGEWVKE 180
DB 121 PAIFKYSCEIIVTHFFPDEQNSMKLGTTWTYDGSVVAINPESQDPDLNFMESGEWVKE 200
QY 181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
DB 201 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 230

RESULT 2
AAI56386
ID AAI56386 standard; Protein; 457 AA.
XX
XX AC AAI56386;
XX
XX 14-FEB-2000 (first entry)
XX
XX DE Human acetylcholine receptor protein sequence.
XX
XX KW Human; acetylcholine receptor; AChR; immune response; allergy;
XX antibody-mediated disease; gene replacement therapy; T cell epitope;
XX dermatological; immunosuppressive; antiinflammatory; haemostatic;
XX antianaemic; antiallergic; antiasthmatic; antithyroid; antidiabetic;
XX autoimmune disease; allergic disease.
XX
XX OS Homo sapiens.
XX
XX PN WO9930736-A2.
XX
XX PD 24-JUN-1999.
XX
XX PF 16-DEC-1998; 98WO-US26787.

XX
XX 16-DEC-1997; 97US-0991143.
XX (MINU ) UNIV MINNESOTA.
XX
XX Conti-Fine BM;
XX
XX WPI; 2000-038343/03.
XX
XX DR N-PSDB; AAZ38821.
XX
XX PT Use of T cell epitope peptides for, e.g. preventing allergies -
XX
XX PS Example 2; Page 219-221; 221pp; English.
XX
XX CC The present invention describes a method for preventing or inhibiting an
XX indication or disease associated with aberrant, pathogenic or undesirable
XX antibody production, particularly autoimmune or allergic diseases. The
XX method comprises administering a T cell epitope peptide. The sequence of
XX the epitope peptide comprises an immunodominant T cell epitope sequence
XX which is less than the sequence of the antigen. The antigen comprises
XX the immunodominant T cell epitope sequence. The method can be used to
XX specifically tolerate or down regulate the priming or activity of
XX antigen-specific T cells of a mammal. It can be used to prevent or
XX inhibit an indication or disease associated with antibody production to
XX an antigen such as an endogenous antigen, e.g. acetylcholine receptor,
XX insulin, growth hormone, factor VIII or factor IX, or an exogenous
XX antigen e.g. a fungal antigen, a plant antigen, an antigen of a domestic
XX cat or an antigen of a mite. It can be used to treat autoimmune diseases,
XX e.g. myasthenia gravis, systemic lupus erythematosus (SLE), Grave's
XX disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,
XX autoimmune asthma, cryoglobulinaemia, thrombotic thrombocytopenic purpura,
XX primary biliary sclerosis, pernicious anaemia or pemphigus. It can be
XX used for treating allergic diseases, e.g. allergic rhinitis, allergic
XX asthma, atopic dermatitis, allergic gastroenteropathy, anaphylaxis
XX urticaria or angioedema. It can also be used in gene therapy for treating
XX a disease such as haemophilia or diabetes or an indication such as
XX adenosine deaminase deficiency, growth hormone deficiency, insulin
XX deficiency, factor IX deficiency or factor VIII deficiency. The present
XX sequence represents human acetylcholine receptor which is used in the
XX exemplification of the present invention.
XX
XX SQ Sequence 457 AA;

Query Match 99.7%; Score 1139; DB 21; Length 457;
Best Local Similarity 99.5%; Pred. No. 2.3e-110;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDVNOQIVTTNVRKQOW 60
DB 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDVNOQIVTTNVRKQOW 80
QY 61 VDYNLKWNPDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIYKFTKVLQYTGHTWTP 120
DB 61 VDYNLKWNPDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIYKFTKVLQYTGHTWTP 140
QY 121 PAIFKYSCEIIVTHFFPDEQNSMKLGTTWTYDGSVVAINPESQDPDLNFMESGEWVKE 180
DB 141 PAIFKYSCEIIVTHFFPDEQNSMKLGTTWTYDGSVVAINPESQDPDLNFMESGEWVKE 200
QY 181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
DB 201 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 230

RESULT 3
AAU69151
ID AAU69151 standard; Protein; 437 AA.
XX
XX AC AAU69151;
XX
XX 29-JAN-2002 (first entry)
XX
XX DE Human Acetylcholine receptor alpha subunit.

```

XX Human; epitope; autoimmune disease; myasthenia gravis;
KW Human leukocyte antigen; acetylcholine receptor; HLA DR3; HLA DR2; AChR;
KW antigen; immunosuppressive; major histocompatibility complex; MHC.
XX Homo sapiens.
XX WO200174848-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10450.
XX 31-MAR-2000; 2000US-193745P.
XX (CORI-) CORIXA CORP.
XX Deshpande S, Spack E, Wehner N, Arimilli S;
XX WPI; 2001-648547/74.
XX Peptide epitopes of the acetylcholine receptor target helper T cells
PT recognize an antigen in association with an MHC component and are
PT useful to treat autoimmune disease particularly myasthenia gravis -
XX Example 1; Fig 1; 46pp; English.
XX The invention relates to a composition comprising an isolated
CC acetylcholine receptor (AChR) oligopeptide of about 12 to 20 amino
CC acids. The peptides form a set of 69 overlapping antigenic peptide
CC epitopes which show various affinities for human leukocyte antigens
CC (HLA) HLA-DR2 and DR3. Also included is a composition comprising an
CC antigenic peptide and a Major histocompatibility complex (MHC) component
CC having an antigenic binding site, where binding of the peptide to
CC the binding site induces non-responsiveness in a target T cell in a
CC mammal, where the MHC component is an MHC class II component. Peptides
CC with affinity for HLA-DR2 and DR-3 from proteins other than AChR are also
CC included. The composition is used to treat myasthenia gravis and other
CC autoimmune diseases. The present sequence is the human acetylcholine
CC receptor from which the 69 antigenic peptide epitopes are derived.
XX
SQ Sequence 437 AA;
Query Match 99.1%; Score 1133; DB 22; Length 437;
Best Local Similarity 99.0%; Pred. No. 9.1e-110;
Matches 208; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNRLKQOW 60
Db 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNRLKQOW 60
QY 61 VDYNLKNPDDYGGVKKIHIPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHITWTP 120
Db 61 VDYNLKNPDDYGGVKKIHIPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHITWTP 120
QY 121 PAIFKSCYEIVTHFPFDEQNCMKLTWTYDGSVAINPESQDPLSNFMESGEWIK 180
Db 121 PAIFKSCYEIVTHFPFDEQNCMKLTWTYDGSVAINPESQDPLSNFMESGEWIK 180
QY 181 SRGKHSVTYSCCPDTPDYITHFVQRL 210
Db 181 SRGKHSVTYSCCPDTPDYITHFVQRL 210
RESULT 4
AAW83381
ID AAW83381 standard; Protein; 235 AA.
XX AAW83381;
XX 19-FEB-1999 (first entry)
XX Human acetylcholine receptor alpha-subunit variant 1.

XX Human; acetylcholine receptor alpha-subunit; hAChR; variant;
KW myasthenia gravis; autoimmune response; neuromuscular disorder;
KW diagnosis.
XX Homo sapiens.
XX Synthetic.
XX WO9850544-A1.
XX 12-NOV-1998.
XX 06-MAY-1998; 98WO-IL00211.
XX 07-MAY-1997; 97IL-0120792.
XX (YEDA) YEDA RES & DEV CO LTD.
XX Barchan D, Fuchs S, Souroujon MC;
XX WPI; 1998-610383/51.
XX N-PSDB; AAV72829.
XX Poly peptide(s) modulating auto-immune response to acetylcholine
PT receptor - comprise all or part of extracellular domain of human
PT acetylcholine receptor alpha-sub:unit, useful in treatment and
PT diagnosis of myasthenia gravis
XX Claim 11; Fig -; 58pp; English.
XX The present sequence represents a human acetylcholine receptor (hAChR)
CC alpha-subunit variant which is used as all or part of a protein for
CC modulating the autoimmune response of an individual to hAChR. The
CC protein can be administered to alleviate and/or treat myasthenia gravis
CC (MG), and is useful for diagnosing the condition. It can be combined
CC with a suitable carrier in pharmaceutical compositions, and is useful
CC for such therapeutic (especially nasal or oral) administration and
CC diagnosis. MG is a human neuromuscular disorder, in which autoantibodies
CC against AChR bind to the receptor and interfere with signal transmission
CC from nerve to muscle at the neuromuscular junction. The extracellular
CC domain of the AChR alpha-subunit appears to be the prime target for
CC these autoantibodies, particularly the main immunogenic region (MIR).
CC The protein enables antigen-specific immunotherapy which suppresses only
CC adverse autoimmune responses whilst leaving overall immune system
CC intact, unlike current methods of treating MG using immunosuppressive
CC drugs e.g. steroids.
CC N.B. The present sequence is not given in the specification but has been
CC created by the indexer as specified in the claim using the sequences
CC given in the figures.
XX SQ Sequence 235 AA;
Query Match 97.2%; Score 1111.5; DB 19; Length 235;
Best Local Similarity 88.5%; Pred. No. 6.7e-108;
Matches 208; Conservative 1; Mismatches 1; Indels 25; Gaps 1;
QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNRLKQ-- 58
Db 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNRLKQGD 60
QY 59 -----QWVDYNLKNPDDYGGVKKIHIPSEKIRPDLVLYNN 95
Db 61 MVDLPRPSCVTGLGVPLFSLHQDEQWVDYNLKNPDDYGGVKKIHIPSEKIRPDLVLYND 120
QY 96 ADGDFALVKTFTKVLQYTGHITWTPPAIFKSCYEIVTHFPFDEQNCMKLTWTYDGSV 155
Db 121 ADGDFALVKTFTKVLQYTGHITWTPPAIFKSCYEIVTHFPFDEQNCMKLTWTYDGSV 180
QY 156 VAINPESQDPLSNFMESGEWIKESRGWKHSVTYSCCPDTPDYITHFVQRL 210
Db 181 VAINPESQDPLSNFMESGEWIKESRGWKHSVTYSCCPDTPDYITHFVQRL 235

RESULT 5

AA06254
ID AAR06254 standard; protein; 456 AA.
XX
AC AAR06254;
XX
DT 07-DEC-1990 (first entry)
XX
DE Human acetylcholine receptor TE671 (AChR) alpha-subunit.
XX
KW Nicotinic acetyl choline receptor; AChR; TE671; insecticides;
KW Muscle relaxants; anthelmintics;
XX
OS Homo sapiens.
XX
PN CA2003459-A.
XX
PD 23-MAY-1990.
XX
PF 21-NOV-1989; 89CA-2003459.
XX
PR 23-NOV-1988; 88US-0275422.
XX
PA (SALK) SALK INST FOR BIOL STUD.
XX
PI Lindstrom JM, Schoepfer RD;
XX
XX WPI; 1990-231525/31.
XX
PT Human muscle nicotinic acetylcholine receptor - used to assay
PT the effects of agents which affect acetylcholine receptors in
PT skeletal muscles.
XX
PS Disclosure; ; p; English.
XX
CC Receptors may be used in assay for materials which modify them.
CC They may be produced in substantial, pure quantities for use in
CC experimentation, development of insecticides without effect on
CC hmnars and treatment of parasitic infections. MABS raised to the
CC peptides may be useful in detection of the structure of MNARS.
CC 24 unidentified residues are due to the poor quality of the
CC sequence reproduction.
XX
SQ Sequence 456 AA;

Query Match 96.3%; Score 1100.5; DB 11; Length 456;
Best Local Similarity 97.1%; Pred. No. 2.4e-106;
Matches 204; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

OY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLQLINVDENVQIVTNNVRLKQW 60
DB 21 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLQLINVDENVQIVTNNVRLKQW 80
OY 61 VDYNLKNPDDYGGVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
DB 81 VDYNLKNPDDYGG-KIHPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 139
OY 121 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESEGWVKE 180
DB 140 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESEGWVKE 199
OY 181 SRGWKHSVTYSCCPDTPYLDITYHFVQRL 210
DB 200 SRGWKHSVTYSCCPDTPYLDITYHFVQRL 229

RESULT 6

AAW83382
ID AAW83382 standard; Protein; 230 AA.
XX
AC AAW83382;
XX
DT 19-FEB-1999 (first entry)

XX

Human acetylcholine receptor alpha-subunit variant 2.

DE

Human; acetylcholine receptor alpha-subunit; hAChR; variant;
KW myasthenia gravis; autoimmune response; neuromuscular disorder;
KW diagnosis.

XX

Homo sapiens.

OS

Synthetic.

OS

WO9850544-A1.

PN

12-NOV-1998.

PD

06-MAY-1998; 98WO-IL00211.

XX

07-MAY-1997; 97IL-0120792.

PR

(YEDA) YEDA RES & DEV CO LTD.

XX

Barchan D, Fuchs S, Souroujon MC;

PI

WPI; 1998-610383/51.

DR

N-PSDB; AAV72830.

XX

Poly-peptide(s) modulating auto-immune response to acetylcholine
receptor - comprise all or part of extracellular domain of human
acetylcholine receptor alpha-subunit, useful in treatment and
diagnosis of myasthenia gravis

XX

Claim 111; Fig -; 58pp; English.

PS

XX

The present sequence represents a human acetylcholine receptor (hAChR)
alpha-subunit variant which is used as all or part of a protein for
modulating the autoimmune response of an individual to hAChR. The
protein can be administered to alleviate and/or treat myasthenia gravis
(MG), and is useful for diagnosing the condition. It can be combined
with a suitable carrier in pharmaceutical compositions, and is useful
for such therapeutic (especially nasal or oral) administration and
diagnosis. MG is a human neuromuscular disorder, in which autoantibodies
against AChR bind to the receptor and interfere with signal transmission
from nerve to muscle at the neuromuscular junction. The extracellular
domain of the AChR alpha-subunit appears to be the prime target for
these autoantibodies, particularly the main immunogenic region (MIR).
The protein enables antigen-specific immunotherapy which suppresses only
adverse autoimmune responses whilst leaving overall immune system
intact, unlike current methods of treating MG using immunosuppressive
drugs e.g. steroids.
N.B. the present sequence is not given in the specification but has been
created by the Indexer as specified in the claim using the sequences
given in the figures.

SQ Sequence 230 AA;

Query Match 95.2%; Score 1088.5; DB 19; Length 230;
Best Local Similarity 88.3%; Pred. No. 1.7e-105;
Matches 203; Conservative 1; Mismatches 1; Indels 25; Gaps 1;

OY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLQLINVDENVQIVTNNVRLKQ-- 58
DB 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLQLINVDENVQIVTNNVRLKQGD 60
OY 59 -----QWVDYNLKNPDDYGGVKKIHPSEKIRPDLVLYNN 95
DB 61 MVDLPRPSCVTILGVPLFSLQLQDEQWVDYNLKNPDDYGGVKKIHPSEKIRPDLVLYND 120
OY 96 ADGDFAIKFTKVLQYTGHTWTPPAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSV 155
DB 121 ADGDFAIKFTKVLQYTGHTWTPPAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSV 180
OY 156 VAINPESDQDPLSNFMESEGWVKEGRGWKHSVTYSCCPDTPYLDITYHF 205
DB 181 VAINPESDQDPLSNFMESEGWVKEGRGWKHSVTYSCCPDTPYLDITYHF 230

RESULT 7

AAR06256
ID AAR06256 standard; protein; 456 AA.

XX AC AAR06256;
XX
DT 07-DEC-1990 (first entry)
XX
XX Calf acetylcholine receptor (Achr) alpha-subunit.
XX
XX Nicotinic acetyl choline receptor; AchR; TE671; insecticides;
KW Muscle relaxants; anthelmintics;
XX

OS Bos taurus.

PN CA2003459-A.

PD 23-MAY-1990.

XX 21-NOV-1989; 89CA-2003459.

XX 23-NOV-1988; 88US-0275422.

PA (SALK) SALK INST FOR BIOL STUD.

XX Lindstrom JM, Schoepfer RD;

XX WPI; 1990-231525/31.

XX Human muscle nicotinic acetyl:choline receptor - used to assay
PT the effects of agents which affect acetyl:choline receptors in
PT skeletal muscles.

XX Disclosure; ; p; English.

XX Receptors may be used in assay for materials which modify them.
CC They may be produced in substantial, pure quantities for use in
CC experimentation, development of insecticides without effect on
CC hMNARS and treatment of parasitic infections. Mabs raised to the
CC peptides may be useful in detection of the structure of MNARS.
CC 24 unidentified residues are due to the poor quality of the
CC sequence reproduction.

XX SQ Sequence 456 AA;

Query Match 95.1%; Score 1086.5; DB 11; Length 456;
Best Local Similarity 95.7%; Pred. No. 7.1e-105;
Matches 201; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVETAGLQIQLINVDENVQIVTTNVRKQOW 60
DB 21 SEHETRLVAKLFKDYSSVVRPVEDHRQVETAGLQIQLINVDENVQIVTTNVRKQOW 80
QY 61 VDYNLKWNPDYGGVKKTHIPSEKIWRPDLVLYNNADGDFAIKFKVLLQYTGHTWTP 120
DB 81 VDYNLKWNPDYGGVKKTHIPSEKIWRPDLVLYNNADGDFAIKFKVLLQYTGHTWTP 139
QY 121 PAIFKSYCEIIVTHPPFQNCMKLGTWYDGSVVAINPESDQDPLSNFMESEGEWVKE 180
DB 140 PAIFKSYCEIIVTHPPFQNCMKLGTWYDGSVVAINPESDQDPLSNFMESEGEWVKE 199
QY 181 SRGWKHSVYTSCCPDTPYLDITYHFVMQRL 210
DB 200 SRQWKHSVYTSCCPDTPYLDITYHFVMQRL 229

RESULT 8

AAR06255
ID AAR06255 standard; protein; 456 AA.

XX AC AAR06255;

XX

DT 07-DEC-1990 (first entry)

XX Mouse acetylcholine receptor (Achr) alpha-subunit.

XX Nicotinic acetyl choline receptor; AchR; TE671; insecticides;
KW Muscle relaxants; anthelmintics;
XX

OS Mus sp.

PN CA2003459-A.

PD 23-MAY-1990.

XX 21-NOV-1989; 89CA-2003459.

XX 23-NOV-1988; 88US-0275422.

PA (SALK) SALK INST FOR BIOL STUD.

XX Lindstrom JM, Schoepfer RD;

XX WPI; 1990-231525/31.

XX Human muscle nicotinic acetyl:choline receptor - used to assay
PT the effects of agents which affect acetyl:choline receptors in
PT skeletal muscles.

XX Disclosure; ; p; English.

XX Receptors may be used in assay for materials which modify them.
CC They may be produced in substantial, pure quantities for use in
CC experimentation, development of insecticides without effect on
CC hMNARS and treatment of parasitic infections. Mabs raised to the
CC peptides may be useful in detection of the structure of MNARS.
CC 24 unidentified residues are due to the poor quality of the
CC sequence reproduction.

XX SQ Sequence 456 AA;

Query Match 94.0%; Score 1074.5; DB 11; Length 456;
Best Local Similarity 93.8%; Pred. No. 1.3e-103;
Matches 197; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVETAGLQIQLINVDENVQIVTTNVRKQOW 60
DB 21 SEHETRLVAKLFKDYSSVVRPVEDHRQVETAGLQIQLINVDENVQIVTTNVRKQOW 80
QY 61 VDYNLKWNPDYGGVKKTHIPSEKIWRPDLVLYNNADGDFAIKFKVLLQYTGHTWTP 120
DB 81 VDYNLKWNPDYGGVKKTHIPSEKIWRPDLVLYNNADGDFAIKFKVLLQYTGHTWTP 139
QY 121 PAIFKSYCEIIVTHPPFQNCMKLGTWYDGSVVAINPESDQDPLSNFMESEGEWVKE 180
DB 140 PAIFKSYCEIIVTHPPFQNCMKLGTWYDGSVVAINPESDQDPLSNFMESEGEWVKE 199
QY 181 SRGWKHSVYTSCCPDTPYLDITYHFVMQRL 210
DB 200 SRQWKHSVYTSCCPDTPYLDITYHFVMQRL 229

RESULT 9

AAR06257
ID AAR06257 standard; protein; 455 AA.

XX AC AAR06257;

XX 07-DEC-1990 (first entry)

XX Chicken acetylcholine receptor (Achr) alpha-subunit.

XX Nicotinic acetyl choline receptor; AchR; TE671; insecticides;
KW Muscle relaxants; anthelmintics;

XX OS Gallus sp.
 XX PN CA2003459-A.
 XX PD 23-MAY-1990.
 XX PF 21-NOV-1989; 89CA-2003459.
 XX PR 23-NOV-1988; 88US-0275422.
 XX PA (SALK) SALK INST FOR BIOL STUD.
 XX PI Lindstrom JM, Schoepfer RD;
 XX WPI; 1990-231525/31.
 XX DR Human muscle nicotinic acetylcholine receptor - used to assay
 PT the effects of agents which affect acetylcholine receptors in
 PT skeletal muscles.
 XX PS Disclosure; ; p; English.
 XX CC Receptors may be used in assay for materials which modify them.
 CC They may be produced in substantial, pure quantities for use in
 CC experimentation, development of insecticides without effect on
 CC hmnars and treatment of parasitic infections. Mabs raised to the
 CC peptides may be useful in detection of the structure of MNARS.
 CC 22 unidentified residues are due to the poor quality of the
 CC sequence reproduction.
 XX Sequence 455 AA;
 SQ
 Query Match 84.8%; Score 969.5; DB 11; Length 455;
 Best Local Similarity 84.2%; Pred. No. 1.2e-92;
 Matches 176; Conservative 16; Mismatches 16; Indels 1; Gaps 1;
 QY 2 EHETRLVAKLFKDYSSVVRPVEDHQRQVETAGLQILQINDEVNQIVTTNVLKQOW 61
 DB 21 EHETRLVAKLFKDYSSVVRPVEDHQRQVETAGLQILQINDEVNQIVTTNVLKQOW 80
 QY 62 DYLNKWNPDYGGVKVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 121
 DB 81 DYLNKWNPDYGGVKVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 139
 QY 122 AIFKSYCEIIVTHFPDEQNCMKLGTTWYDGSVVAINPESDQPLSNFMESEGWIKES 181
 DB 140 AIFKSYCEIIVTHFPDEQNCMKLGTTWYDGSVVAINPESDQPLSNFMESEGWIKES 199
 QY 182 RGWKHSVTYSCCPDTPYLDITYHFVQMRL 210
 DB 200 RGWKHSVTYSCCPDTPYLDITYHFVQMRL 228
 RESULT 10
 AAR36984
 ID AAR36984 standard; Protein; 449 AA.
 XX AC AAR36984;
 XX DT 24-SEP-1993 (first entry)
 XX DE Acetylcholine receptor protein, alpha subunit.
 KW Acetylcholine receptor; AChR; epitope; myasthenia gravis; human; MHC;
 KW mouse; MHC-peptide complex; subunit; antigen; binding site; receptor;
 KW T-cell; autoimmune disease; immune system; rheumatoid arthritis;
 KW multiple sclerosis; myasthenia gravis.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Peptide 1..12

FT Protein /note= "signal peptide"
 FT 13..449
 XX /note= "Mature protein"
 PN WO9309810-A.
 XX 27-MAY-1993.
 XX 18-NOV-1992; 92WO-US10031.
 XX 19-NOV-1991; 91US-0793938.
 XX (ANER-) ANERGEN INC.
 XX Clark BR, McConnel HM, Nag B, Sharma SD;
 XX WPI; 1993-182250/22.
 DR N-PSDB; AAQ39941.
 XX Complexes comprising antigenic peptide and major
 PT histocompatibility complex sub-unit - for treatment and diagnosis
 PT of immune diseases, e.g. rheumatoid arthritis, multiple sclerosis
 PT and myasthenia gravis
 XX Disclosure; Fig 3; 85pp; English.
 PS This sequence represents the alpha subunit of acetylcholine receptor
 CC protein. This sequence may be used in the construction of an
 CC MHC-peptide complex which comprises an antigenic peptide, eg. AChR
 CC peptide 193-215 or myelin basic protein peptide MBP(1-14)A4, and an
 CC isolated MHC subunit component which has an antigen binding site,
 CC where the antigenic peptide is associated with the antigen binding
 CC site. The MHC-peptide complex selectively binds a T-cell receptor
 CC on T-cells associated with diseases, esp. autoimmune diseases. The
 CC coding sequence of this protein may be incorporated in to a sequence
 CC encoding the subunit derived from the MHC antigen. The incorporated
 CC site will be such that, when the subunit is expressed and folded, the
 CC AChR peptide antigen will be available as an epitope for the target
 CC T-cells. The complex may be used to identify and inhibit aspects of
 CC the immune system which are responsible for undesirable immune
 CC responses. They may be used for treating autoimmune disease such as
 CC rheumatoid arthritis, multiple sclerosis or myesthenia gravis.
 XX Sequence 449 AA;
 SQ
 Query Match 79.6%; Score 910; DB 14; Length 449;
 Best Local Similarity 75.2%; Pred. No. 2e-86;
 Matches 158; Conservative 26; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEHETRLVAKLFKDYSSVVRPVEDHQRQVETAGLQILQINDEVNQIVTTNVLKQOW 60
 DB 13 SEHETRLVAKLFKDYSSVVRPVEDHQRQVETAGLQILQINDEVNQIVTTNVLKQOW 72
 QY 61 DYLNKWNPDYGGVKVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
 DB 73 DYLNKWNPDYGGVKVKKIHPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 132
 QY 121 PAIFKSYCEIIVTHFPDEQNCMKLGTTWYDGSVVAINPESDQPLSNFMESEGWIKES 180
 DB 133 PAIFKSYCEIIVTHFPDEQNCMKLGTTWYDGSVVAINPESDQPLSNFMESEGWIKES 192
 QY 181 SRGWKHSVTYSCCPDTPYLDITYHFVQMRL 210
 DB 193 SRGWKHSVTYSCCPDTPYLDITYHFVQMRL 222
 RESULT 11
 AAR86421
 ID AAR86421 standard; Protein; 449 AA.
 XX AC AAR86421;
 XX DT 10-APR-1996 (first entry)


```
XX DE Acetylcholine receptor alpha subunit.
XX DE
XX DE Acetylcholine receptor; autoantigen; MHC class II;
KW major histocompatibility complex; autoimmunity; autoimmune disease;
KW rheumatoid arthritis; myasthenia gravis; multiple sclerosis;
KW allograft rejection; vaccine.
XX OS
XX OS Torpedo californicus.
XX PN
XX PN US5468481-A.
XX PD
XX PD 21-NOV-1995.
XX PF
XX PF 23-JUN-1988; 88US-0210594.
XX PR
XX PR 14-APR-1992; 92US-0869293.
XX PR 23-JUN-1988; 88US-0210594.
XX PR 21-JUN-1989; 89US-0367751.
XX PR 30-AUG-1990; 90US-0576084.
XX PR 28-DEC-1990; 90US-0635840.
XX PR 23-APR-1991; 91US-0690840.
XX PA
XX PA (AMER-) AMERGEN INC.
XX PI
XX PI Clark BR, Lerch BL, Sharma SD;
XX WPI; 1996-010049/01.
XX DR N-PSDB; AAT06284.
XX PT
XX PT New MHC Class 2-peptide complex for inducing T cell
XX non-responsiveness - opt. including a toxin, esp. for treating
XX auto-immune disease such as rheumatoid arthritis
XX PS
XX PS Disclosure; Fig 6; 47pp; English.
XX CC
XX CC The alpha subunit of the electric ray acetylcholine receptor (AChR)
XX (AAR6421) is an autoantigen involved in the pathogenesis of myasthenia
XX gravis. AChR peptide segments, e.g. amino acids 195-215, can be used
XX in the construction of MHC class II-peptide conjugates. Such
XX conjugates are able to inhibit deleterious T-cell mediated immune
XX response, such as allergic reactions, allograft rejection, and
XX autoimmune diseases, or to promote T-cell responses for use as
XX vaccines.
XX SQ
XX SQ Sequence 449 AA;
Query Match 79.6%; Score 910; DB 17; Length 449;
Best Local Similarity 75.2%; Pred. No. 2e-86;
Matches 158; Conservative 26; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEHETRLVAKLFKDYSSVRPVEDHROVVEVTAGLQLIQLINVDVQIVTNNVRLKQOW 60
DB 13 SEHETRLVANLLENYKVRPVEHHTFVDITVGLQLIQLISVDVQIVETNVRRLQOW 72
QY 61 VDNLKNWPDYGGVKKIHIPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHTITWTP 120
DB 73 IDVRLRNWPDYGGKIKIRLPDSDVWLPDLVLYNNADGDFAIKFTKVLQYTGHTITWTP 132
QY 121 PAIFKSCYELIVTHFPFDEQNCMKLTWTYDGSVVAINPESDQDLSNEMESGEWVKE 180
DB 133 PAIFKSCYELIVTHFPFDEQNCMKLTWTYDGSVVAINPESDQDLSNEMESGEWVKE 192
QY 181 SRGKKHSVYSCCPDTPYLDITYHFVQRL 210
DB 193 YRGWKHWVYTCPPDTPYLDITYHFVQRI 222
RESULT 12
AAP40417
ID AAP40417 standard; protein; 461 AA.
XX
XX
AC AAP40417;
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```
XX XX 22-JUL-1992 (first entry)
XX DE Acetyl choline acceptor protein.
XX KW Peptides; immunogenic.
XX OS
XX OS Homo sapiens.
XX FH
XX FH Key Location/Qualifiers
XX Region 1..24
XX Peptide /label= signal_peptide
XX Peptide 25..30
XX Peptide /note= "Immunogenic peptide"
XX Peptide 98..103
XX Peptide /note= "Immunogenic peptide"
XX Peptide 95..100
XX Peptide /note= "Immunogenic peptide"
XX Peptide 103..108
XX Peptide /note= "Immunogenic peptide"
XX Peptide 108..113
XX Peptide /note= "Immunogenic peptide"
XX Peptide 175..180
XX Peptide /note= "Immunogenic peptide"
XX Peptide 192..196
XX Peptide /note= "Immunogenic peptide"
XX Peptide 209..214
XX Peptide /note= "Immunogenic peptide"
XX Peptide 251..256
XX Peptide /note= "Immunogenic peptide"
XX Peptide 315..320
XX Peptide /note= "Immunogenic peptide"
XX Peptide 344..354
XX Peptide /note= "Immunogenic peptide"
XX Peptide 381..387
XX Peptide /note= "Immunogenic peptide"
XX Peptide 401..406
XX Peptide /note= "Immunogenic peptide"
XX JP59130254-A.
XX 26-JUL-1984.
XX 16-AUG-1983; 83JP-0523787.
XX 16-AUG-1983; 83US-0523787.
XX (MITU ) MITSUBISHI CHEM IND KK.
XX WPI; 1984-265833/43.
XX New polypeptide(s) - with immuno activity similar to acetyl choline
XX acceptor
XX Disclosure; Fig 1; 12pp; Japanese.
XX The polypeptides have immunoactivity similar to that of the acetyl
XX choline acceptor. They may be prepd. by solid phase synthesis.
XX SQ
XX SQ Sequence 461 AA;
Query Match 79.6%; Score 910; DB 5; Length 461;
Best Local Similarity 75.2%; Pred. No. 2.1e-86;
Matches 158; Conservative 26; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEHETRLVAKLFKDYSSVRPVEDHROVVEVTAGLQLIQLINVDVQIVTNNVRLKQOW 60
DB 25 SEHETRLVANLLENYKVRPVEHHTFVDITVGLQLIQLISVDVQIVETNVRRLQOW 84
QY 61 VDNLKNWPDYGGVKKIHIPSEKIRPDLVLYNNADGDFAIKFTKVLQYTGHTITWTP 120
DB 85 IDVRLRNWPDYGGKIKIRLPDSDVWLPDLVLYNNADGDFAIKFTKVLQYTGHTITWTP 144
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QY 121 PAIFKSYCEIIVTHFPFDRQNSMKLGITWTYDGSVVAINPESDQPDLSNFMESGEWVKE 180
 DB 145 PAIFKSYCEIIVTHFPFDRQNSMKLGITWTYDGSVVAINPESDQPDLSNFMESGEWVKE 204
 QY 181 SRGWKHSVTYSCPDTPYLDITYHFVMOQL 210
 DB 205 YRGWKHWWYTCPPDTPYLDITYHFIMQRI 234

RESULT 13
 AAR35057
 ID AAR35057 standard; Protein; 449 AA.
 XX AAR35057;
 AC AAR35057;
 DT 21-MAY-1993 (first entry)
 DE Alpha subunit of Torpedo californicus AChR (known).
 XX
 KW Acetylcholine receptor; epitope; myasthenia gravis; MG; antigen;
 binding site; MHC; IAB; alpha; beta; RAMPS; Torpedo californicus.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..12
 FT /label= sig_peptide
 FT Protein 13..449
 FT /label= mat_protein
 XX
 PN W09218150-A.
 XX
 PD 29-OCT-1992.
 XX
 PF 23-APR-1992; 92WO-US03391.
 XX
 PR 23-APR-1991; 91US-0690840.
 XX
 PA (ANER-) ANERGEN INC.
 XX
 PI Clark BR, Lerch BL, Sharma SD;
 XX
 DR WPI; 1993-036056/04.
 DR N-PSDB; AAQ35053.
 XX
 PT Pure major MHC-peptide complex - useful in treating deleterious
 immune response such as auto:immunity
 XX
 PS Disclosure; Fig 6; 93pp; English.
 XX
 CC The Dupont apparatus and technique for rapid multiple peptide
 synthesis (RAMPS) is used to synthesise the members of a set of
 overlapping (10 residue overlap), 20 residue peptides form the alpha
 subunit of Torpedo californicus AChR.
 CC
 CC The AChR peptide 195-215, which has been characterised as an epitope
 in myasthenia gravis (MG) in humans and in mice, may be connected to
 the N-terminal antigen binding site of a polypeptide derived from an MHC
 antigen associated with MG. For example, if the recombinant complex is
 to be used in mice, the AChR peptide may be incorporated into a sequence
 encoding either the I-Ab-alpha or I-Ab-beta chain (see AAQ35054-55
 respectively). If the AChR peptide is to be incorporated into the beta
 chain, for example, the oligonucleotide may be inserted as a replacement
 for the leader sequence.

XX Sequence 449 AA;
 SQ
 Query Match 79.08; Score 903; DB 14; Length 449;
 Best Local Similarity 74.8; Pred. No. 1.le-85;
 Matches 157; Conservative 26; Mismatches 27; Indels 0; Gaps 0;
 QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLIQLINVDVNOIVTNNRLKQOW 60
 DB 13 SEHETRLVANLENNYKVIPIPPVEHHTHFVDITVGLQLQLISVDVNOIVETNRLRQOW 72

QY 61 VDYNLKWNPPDDYGGVKKIHPSEKIWRPDLVLYNNADGFAIVKFTKVLQYTGHTTWP 120
 DB 73 IDVRLRNWPNADYGGIKIRLPSSDDVWLPLVLYNNADGFAIVHMTKLLDYTGKIMWTP 132
 QY 121 PAIFKSYCEIIVTHFPFDRQNSMKLGITWTYDGSVVAINPESDQPDLSNFMESGEWVKE 180
 DB 133 PAIFKSYCEIIVTHFPFDRQNSMKLGITWTYDGSVVAINPESDQPDLSNFMESGEWVKE 192
 QY 181 SRGWKHSVTYSCPDTPYLDITYHFVMOQL 210
 DB 193 YRGWKHWWYTCPPDTPYLDITYHFIMQRI 222

RESULT 14
 AAR45946
 ID AAR45946 standard; Protein; 449 AA.
 XX AAR45946;
 AC AAR45946;
 DT 08-JUL-1994 (first entry)
 DE Acetylcholine receptor alpha subunit.
 XX
 KW MHC; major histocompatibility complex; toxic conjugate;
 autoimmunity; autoimmune disease; helper T-cell; T-lymphocyte;
 acetylcholine receptor; myelin basic protein; I-Ab.
 XX
 OS Torpedo californicus.
 XX
 PN US5284935-A.
 XX
 PD 08-FEB-1994.
 XX
 PF 23-JUN-1988; 88US-0210594.
 XX
 PR 23-JUN-1988; 88US-0210594.
 PR 21-JUN-1989; 89US-0367751.
 PR 30-AUG-1990; 90US-0576084.
 PR 28-DEC-1990; 90US-0635840.
 XX
 PA (ANER-) ANERGEN INC.
 XX
 PI Clark BR, Lerch LB, Sharma SD;
 XX
 DR WPI; 1994-056406/07.
 DR N-PSDB; AAQ56918.
 XX
 PT MHC-mediated toxic peptide conjugates - useful for ameliorating
 auto-immunity
 XX
 PS Disclosure; Fig 6.1-6.4; 42pp; English.
 XX
 CC The acetylcholine receptor alpha subunit given in sequence AAR45946
 (corresponding mRNA in AAQ56918) and the myelin basic protein given in
 AAR45947 are antigenic peptides associated with autoantigens. They
 have been conjugated with MHC class II components such as I-Ab-
 alpha chain (encoded by MHC class II components such as I-Ab-
 alpha chain (encoded by sequence AAQ56919) or I-Ab-beta chain,
 (encoded by AAQ56920) and a toxin or label to form conjugates used
 to target helper T-cells for the treatment of autoimmune diseases.

XX Sequence 449 AA;
 SQ
 Query Match 77.48; Score 885; DB 15; Length 449;
 Best Local Similarity 74.48; Pred. No. 8.2e-84;
 Matches 157; Conservative 26; Mismatches 26; Indels 2; Gaps 2;
 QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLIQLINVDVNOIVTNNRLKQOW 60
 DB 13 SEHETRLVANLENNYKVIPIPPVEHHTHFVDITVGLQLQLISVDVNOIVETNRLRQOW 72
 QY 61 VDYNLKWNPPDDYGGVKKIHPSEKIWRPDLVLYNNADGFAIVKFTKVLQYTGHTTWP 119
 DB 73 IDVRLRNWPNADYGGIKIRLPSSDDVWLPLVLYNNADGFAIVHMTKLLDYTGKIMWTP 132

Db 73 IDVRLRNADYGGIKIRLPDDVWLPDLVLYNNADGDFAIHVHTKLLLDYTGKIMWT 132
Qy 120 PPAIFKSYCEIIVTHFPFDEQNCMKLGWTYDGSVVAINPESDQDLSNFMESGEWIK 179
Db 133 PPAIFKSYCE--IVTHFPDQNCMKLGWTYDGTGKVSISPESDRDLSNFMESGEWYMK 191
Qy 180 ESRGWKHSVTYSCCPDTPYLDITYHFVQMRL 210
Db 192 DYRGWKHWYTCPCDTPYLDITYHFIMQRI 222

RESULT 15

AAR06259
ID AAR06259 standard; protein; 460 AA.

XX AC AAR06259;

XX DT 07-DEC-1990 (first entry)

XX DE Fish acetylcholine receptor (AChR) alpha-subunit.

XX KW Nicotinic acetyl choline receptor; AChR; TE671; insecticides;
XX KW Muscle relaxants; antihelmintics;

XX OS Torpedo sp.

XX PN CA2003459-A.

XX PD 23-MAY-1990.

XX PF 21-NOV-1989; 89CA-2003459.

XX PR 23-NOV-1988; 88US-0275422.

XX PA (SALK) SALK INST FOR BIOL STUD.

XX PI Lindstrom JM, Schoepfer RD;

XX DR WPI; 1990-231525/31.

XX PT Human muscle nicotinic acetyl:choline receptor - used to assay
PT the effects of agents which affect acetyl:choline receptors in
PT skeletal muscles.

XX PS Disclosure; ; P; English.

XX CC Receptors may be used in assay for materials which modify them.
CC They may be produced in substantial, pure quantities for use in
CC experimentation, development of insecticides without effect on
CC hMNARs and treatment of parasitic infections. MABS raised to the
CC peptides may be useful in detection of the structure of MNARs.
CC Unidentified residues are due to the poor quality of the
CC sequence reproduction.

XX SQ Sequence 460 AA;

Query Match 73.9%; Score 845; DB 11; Length 460;
Best Local Similarity 71.9%; Pred. No. 1.3e-79;
Matches 151; Conservative 20; Mismatches 39; Indels 0; Gaps 0;

Qy 1 SEHETRLVAKLFKDYSSVRVPEHVRQVEVTAGLQLQLINVDVNOIVTNNRLKQOW 60
Db 25 SEHETRLVANLKNVIRCEHTEHFDITVGLQLQLISVDVNOIVTNNRLKQOW 84
Qy 61 VDYNLKNPDDYGGVKKIHPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
Db 85 IDVRLRNADYGGIKIRLPDDVWLPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 144
Qy 121 PPAIFKSYCEIIVTHFPFDEQNCMKLGWTYDGSVVAINPESDQDLSNFMESGEWIK 180
Db 145 PPAIFKSYCEIIVTHFPFDEQNCXXLGTWYDGTGKVSINPESDQDLSNFMESGEWIXE 204
Qy 181 SRGWKHSVTYSCCPDTPYLDITYHFVQMRL 210

Db 205 SRGWKHSVTYTCPCDTPYLDITYHFIMQRL 234
Search completed: January 14, 2003, 16:53:40
Job time : 142 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2003, 16:51:18 ; Search time 49 Seconds
(without alignments)
412.005 Million cell updates/sec

Title: US-09-820-339A-2

Perfect score: 1143

Sequence: 1 SEHETRLVAKLFKDYSSVVR.....SCPDTPYLDIYHFVQRL 210

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1139	99.7	457	1 ACHUA1	nicotinic acetylch
2	1096	95.9	445	2 I49458	acetylcholine rece
3	1096	95.9	457	1 ACBOA1	nicotinic acetylch
4	1095	95.8	457	2 S13872	nicotinic acetylch
5	1093	95.6	457	2 A24383	nicotinic acetylch
6	983	86.0	456	1 ACCHAN	nicotinic acetylch
7	915	80.1	255	2 A93440	nicotinic acetylch
8	915	80.1	461	2 I50548	acetylcholine rece
9	910	79.6	461	1 ACRVA1	nicotinic acetylch
10	888	77.7	457	2 A28529	nicotinic acetylch
11	875	76.6	457	2 S08162	nicotinic acetylch
12	594.5	52.0	499	2 A24572	nicotinic acetylch
13	594.5	52.0	503	2 A53956	nicotinic acetylch
14	588.5	51.5	495	2 S60589	acetylcholine rece
15	588.5	51.5	502	2 A37040	nicotinic acetylch
16	582.5	51.0	625	2 A26456	nicotinic acetylch
17	577.5	50.5	627	2 JC4021	nicotinic acetylch
18	574.5	50.3	494	2 T09289	nicotinic acetylch
19	571.5	50.0	512	2 B37014	nicotinic acetylch
20	571.5	50.0	622	1 ACCH4N	nicotinic acetylch
21	571	50.0	468	2 A38223	nicotinic acetylch
22	564.5	49.4	511	2 A01110	nicotinic acetylch
23	564	49.3	452	2 A35721	nicotinic acetylch
24	562.5	49.2	528	1 ACCH2N	nicotinic acetylch
25	553.5	48.4	462	2 S06893	nicotinic acetylch
26	552	48.3	567	1 ACPPA1	nicotinic acetylch
27	544	47.6	454	2 B39218	nicotinic acetylch
28	532.5	46.6	455	2 A55972	nicotinic acetylch
29	532.5	46.6	455	2 S51116	nicotinic acetylch

30	532.5	46.6	454	2 A33523	nicotinic acetylch
31	522.5	45.7	576	1 ACFFA2	nicotinic acetylch
32	520.5	45.5	466	2 S16333	nicotinic acetylch
33	518.5	45.4	423	2 I38056	nicotinic acetylch
34	514.5	45.0	565	2 T23843	hypothetical prote
35	508	44.4	557	2 S12359	nicotinic acetylch
36	503	44.0	500	2 S12899	nicotinic acetylch
37	479	41.9	491	1 ACCHNN	nicotinic acetylch
38	479	41.9	503	2 JH0174	nicotinic acetylch
39	477.5	41.8	521	1 ACFFNN	nicotinic acetylch
40	472	41.3	502	2 S10505	nicotinic acetylch
41	469.5	41.1	479	2 A55382	nicotinic acetylch
42	469	41.0	470	2 A39218	nicotinic acetylch
43	467.5	40.9	511	2 T43634	nicotinic acetylch
44	463.5	40.6	534	2 T25720	hypothetical prote
45	461.5	40.4	416	1 ACCH3N	nicotinic acetylch

ALIGNMENTS

RESULT 1

ACHUA1

nicotinic acetylcholine receptor alpha-1 chain precursor, muscle - human
C;Species: Homo sapiens (man)

C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 22-Jun-1999

C;Accession: A03168; S00238; A27591

R;Noda, M.; Furutani, Y.; Takahashi, H.; Toyosato, M.; Tanabe, T.; Shimizu, S.; Kikyo

Nature 305, 818-823, 1983
A;Title: Cloning and sequence analysis of calf cDNA and human genomic DNA encoding al

A;Reference number: A03168; MUID:84039794; PMID:6688857

A;Accession: A03168

A;Molecule type: DNA

A;Residues: 1-457 <NOD>

A;Cross-references: GB:X02502; NID:g28291; PIDN:CAA26344.1; PID:g669153

R;Schoepfer, R.; Luther, M.; Lindstrom, J.

FEBS Lett. 226, 235-240, 1988

A;Title: The human medulloblastoma cell line TE671 expresses a muscle-like acetylcholin

A;Reference number: S00238; MUID:88112190; PMID:3338555

A;Accession: S00238

A;Molecule type: mRNA

A;Residues: 1-457 <SCH>

A;Cross-references: EMBL:Y00762; NID:g28308; PIDN:CAA68731.1; PID:g28309

R;Hohlfeld, R.; Toyka, K.V.; Miner, L.L.; Walgrave, S.L.; Conti-Tronconi, B.M.

J. Clin. Invest. 81, 657-660, 1988

A;Title: Amphipathic segment of the nicotinic receptor alpha subunit contains epitope

A;Reference number: A27591; MUID:88139764; PMID:2449458

A;Contents: annotation

C;Genetics:

A;Gene: GDB:CHRNA1; CHRNA

A;Cross-references: GDB:120586; OMIM:100690

A;Map position: 2q24-2q32

A;Introns: 15/1; 63/3; 78/3; 115/2; 180/3; 260/1; 334/3; 414/3

C;Complex: the functional receptor molecule is a heteropentamer with two alpha chains

C;Superfamily: acetylcholine receptor

C;Keywords: alternative splicing; glycoprotein; heteropentamer; ion channel; neurotra

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-457/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT

F;231-257/Domain: transmembrane #status predicted <TM1>

F;263-281/Domain: transmembrane #status predicted <TM2>

F;297-318/Domain: transmembrane #status predicted <TM3>

F;429-447/Domain: transmembrane #status predicted <TM4>

F;148-162/Disulfide bonds: #status predicted

F;161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.7%; Score 1139; DB 1; Length 457;

Best Local Similarity 99.5%; Pred. No. 4.7e-97;

Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPEHROVVEVTAGLIQLINVDVNAQIVTTNRLKQOW 60

Db 21 SEHETRLVAKLFKDYSSVVRPEHROVVEVTAGLIQLINVDVNAQIVTTNRLKQOW 80

Qy 61 VDYNLKWPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFKTKVLLQYTGHITWTP 120
|||||
Db 81 VDYNLKWPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFKTKVLLQYTGHITWTP 140
|||||
Qy 121 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESGEWVKE 180
|||||
Db 141 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESGEWVKE 200
|||||

Qy 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
|||||
Db 201 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 230
|||||

RESULT 2

I49458

acetylcholine receptor alpha-subunit - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 30-May-1997

C:Accession: I49458

R:Boulter, J.; Luyten, W.; Evans, K.; Mason, P.; Ballivet, M.; Goldman, D.; Stengelin, S.

J. Neurosci. 5, 2545-2552, 1985

Title: Isolation of a clone coding for the alpha-subunit of a mouse acetylcholine receptor

Reference number: I49458; MUID:85292055; PMID:2993547

A:Accession: I49458

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-445 <RES>

A:Cross-references: GB:M17640; NID:g191601; PID:g191602

C:Superfamily: acetylcholine receptor

C:Keywords: neurotransmitter receptor

Query Match 95.9%; Score 1096; DB 2; Length 445;

Best Local Similarity 94.8%; Pred. No. 4.2e-93;

Matches 199; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNVRLKQW 60
|||||

Db 9 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNVRLKQW 68
|||||

Qy 61 VDYNLKWPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFKTKVLLQYTGHITWTP 120
|||||

Db 69 VDYNLKWPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFKTKVLLQYTGHITWTP 128
|||||

Qy 121 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESGEWVKE 180
|||||

Db 129 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESGEWVKE 188
|||||

Qy 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
|||||

Db 189 ARGKHWVYFSCCPDTPYLDITYHFVMQRL 218
|||||

RESULT 3

ACBOAL

nicotinic acetylcholine receptor alpha chain precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 22-Jun-1999

C:Accession: A03169

R:Noda, M.; Furutani, Y.; Takahashi, H.; Toyosato, M.; Tanabe, T.; Shimizu, S.; Kikuyama

Nature 305, 818-823, 1983

A>Title: Cloning and sequence analysis of calf cDNA and human genomic DNA encoding alpha

A:Reference number: A03168; MUID:84039794; PMID:6688857

A:Accession: A03169

A:Molecule type: mRNA

A:Residues: 1-457 <NOD>

A:Cross-references: GB:X02509; NID:g49; PIDN:CAA26345.1; PID:g50

A>Note: four hydrophobic transmembrane segments are found in each of the four kinds of c

-318, and 429-447 in the alpha chain

C:Comment: The functional receptor molecule has two alpha chains and one each of the bet

C:Superfamily: acetylcholine receptor

C:Keywords: glycoprotein; ion channel; membrane protein; neurotransmitter receptor; post

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-457/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT>

F:148-162/Disulfide bonds: #status predicted
F:161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.9%; Score 1096; DB 1; Length 457;

Best Local Similarity 95.2%; Pred. No. 4.3e-93;

Matches 200; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNVRLKQW 60
|||||

Db 21 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNVRLKQW 80
|||||

Qy 61 VDYNLKWPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFKTKVLLQYTGHITWTP 120
|||||

Db 81 VDYNLKWPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFKTKVLLQYTGHITWTP 140
|||||

Qy 121 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESGEWVKE 180
|||||

Db 141 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESGEWVKE 200
|||||

Qy 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
|||||

Db 201 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 230
|||||

RESULT 4

SI3872

nicotinic acetylcholine receptor alpha chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999

C:Accession: SI3872

R:Witzemann, V.; Stein, E.; Barg, B.; Konno, T.; Koenen, M.; Kues, W.; Criado, M.; Ho

Eur. J. Biochem. 194, 437-448, 1990

A>Title: Primary structure and functional expression of the alpha-, beta-, gamma-, de

A:Reference number: SI3872; MUID:91099317; PMID:1702709

A:Accession: SI3872

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-457 <WIT>

A:Cross-references: EMBL:X74832; NID:g398831; PIDN:CAA52826.1; PID:g398832

C:Superfamily: acetylcholine receptor

Query Match 95.8%; Score 1095; DB 2; Length 457;

Best Local Similarity 94.8%; Pred. No. 5.3e-93;

Matches 199; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNVRLKQW 60
|||||

Db 21 SEHETRLVAKLFKDYSSVVRPVEDHROVVEVTAGLQIQLINVDENVQIVTNNVRLKQW 80
|||||

Qy 61 VDYNLKWPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFKTKVLLQYTGHITWTP 120
|||||

Db 81 VDYNLKWPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFKTKVLLQYTGHITWTP 140
|||||

Qy 121 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESGEWVKE 180
|||||

Db 141 PAIFKSYCEIIVTHPPFDEQNCMKLGTTWYDGSVVAINPESDQDPLSNFMESGEWVKE 200
|||||

Qy 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
|||||

Db 201 ARGKHWVYFSCCPDTPYLDITYHFVMQRL 230
|||||

RESULT 5

A24383

nicotinic acetylcholine receptor alpha chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 15-Jun-1996

C:Accession: A24383

R:Isenberg, K.E.; Mudd, J.; Shah, V.; Merlie, J.P.

Nucleic Acids Res. 14, 5111, 1986

A:Reference number: A24383; MUID:86259081; PMID:3755237

A:Accession: A24383

A:Molecule type: mRNA

Query Match	79.6%;	Score 910;	DB 1;	Length 461;
Best Local Similarity	75.2%;	Pred. No. 6e-76;		
Matches 158;	Conservative 26;	Mismatches 26;	Indels 0;	Gaps 0;
QY	1	SEHETRLVAKLFKDYSVSVRPVEDHROVVEVTAGLQILQINVDVHQIVTNNVRLKQOW	60	
Db	25	SEHETRLVANLLENYKNKVIKRPVEHHTHFVDITVGLQILQISVDVQIVETNVLRLQOW	84	
QY	61	VDYLNKWNDDYGGVKIKHPIPSKIKRNPDLVLYNNADGDFAIVKFTKVLQYTGHIWTWP	120	
Db	85	IDYRLRNPNADYGGIKKIRLPSDDVNLDPDLVLYNNADGDFAIVHMTKLLDYTGKINWTP	144	
QY	121	PAIFKSYCEIIVTHFFPDQONCSMKLGTWTYDGSVAINPESDQPDLSNFMESGEWIKI	180	
Db	145	PAIFKSYCEIIVTHFFPDQONCTMKLGITWTYDGTGVKSIPSDRDPDLSTFMESGEWVWKO	204	
QY	181	SRGWKHSVTYSCCPDTPYLDITYHFMQRL	210	
Db	205	YRGWKHWYVYTCCTPDTPYLDITYHFMQRI	234	

nicotinic acetylcholine receptor alpha chain precursor - Pacific electric ray
Species: torpedo californica (pacific electric ray)
Date: 30-Apr-1982 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C:Accession: A03170; A33555; A41587; A54233
R:Noda, M.; Takahashi, H.; Tanabe, T.; Toyosato, M.; Furutani, Y.; Hirose, T.; Asai, M.
Nature 299, 793-797, 1982
A:Title: Primary structure of alpha-subunit precursor of Torpedo californica acetylcholine receptor
A:Reference number: A93290; MUID:83036943; PMID:6182472
A:Accession: A03170
A:Molecule type: mRNA
A:Residues: 1-461 <ND>
A:Cross-references: GB:M14810; NID:g213217; PIDN:AAA96705.1; PID:g213218
R:Conti-Tronconi, B.M.; Hunkapiller, M.W.; Rafferty, M.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 2631-2634, 1984
A:Title: Molecular weight and structural nonequivalence of the mature alpha subunits of
A:Reference number: A20972; MUID:84194060; PMID:6585820
A:Accession: A20972
A:Molecule type: protein
A:Residues: 25-127;336-421;429-450 <CON>
R:Moore, C.R.; Yates III, J.R.; Griffin, P.R.; Shabanowitz, J.; Martino, P.A.; Hunt, D.
Biochemistry 28, 9184-9191, 1989
A:Title: Proteolytic fragments of the nicotinic acetylcholine receptor identified by mass
A:Reference number: A33555; MUID:90105466; PMID:2605252
A:Accession: A33555

A:Status: preliminary
A:Molecule type: protein
A:Residues: 29-41;82-88;132-149;339-354;363-411 <MOO>
R:Cohen, J.B.; Sharp, S.D.; Liu, W.S.
J. Biol. Chem. 266, 23354-23364, 1991
Title: Structure of the agonist-binding site of the nicotinic acetylcholine receptor.
Reference number: A41587; MUID:92078212; PMID:1744130
Accession: A41587
A:Molecule type: protein
A:Residues: 104-131 <COH>
A:Note: residue 117-Tyr was shown to be alkylated by [3H]-acetylcholine mustard, an analog of acetylcholine.
R:Blanton, M.P.; Cohen, J.B.
Biochemistry 33, 2859-2872, 1994
A:Title: Identifying the lipid-protein interface of the Torpedo nicotinic acetylcholine receptor.
Reference number: A54233; MUID:94176477; PMID:8130199
Accession: A54233

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 234-266;287-319;423-453 <BLA>
 C:Complex: heterotrimer of two alpha chains, one beta chain (see PIR:ACRYB1), one gamma chain
 C:Superfamily: acetylcholine receptor
 C:Keywords: ion channel; membrane protein; neurotransmitter receptor; postsynaptic membrane
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-461/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT>
 F:236-259/Domain: transmembrane #status predicted <TM1>
 F:267-285/Domain: transmembrane #status predicted <TM2>
 F:297-324/Domain: transmembrane #status predicted <TM3>
 F:423-450/Domain: transmembrane #status predicted <TM4>

```

Query Match          77.7%; Score 888; DB 2; Length 457;
Best Local Similarity 75.2%; Pred. No. 6.3e-74;
Matches 158; Conservative 23; Mismatches 29; Indels 0; Gaps 0;

```

[illegible]

RESULT 11
S08162

S08162
 Serotonergic acetylcholine receptor alpha-la chain precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
 C:Accession: S08162
 R:Hartman, D.S.: Claudio, T.
 Nature 343, 372-375, 1990
 A:Title: Coexpression of two distinct muscle acetylcholine receptor alpha-subunits du
 A:Reference number: S08162; MUID:90136925; PMID:2300185
 A:Accession: S08162
 A:Molecule type: mRNA

A;Residues: 1-457 <HAR>
A;Cross-references: EMBL:X17244; NID:g64514; PIDN:CAA35109.1; PID:g64515
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; heteropentamer; ion channel; neurotransmitter receptor; postsynaptic membrane; signal sequence #status predicted <SIG>
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-457/Product: nicotinic acetylcholine receptor alpha-1a chain #status predicted <MAT>
F;231-259/Domain: transmembrane #status predicted <TM1>
F;263-281/Domain: transmembrane #status predicted <TM2>
F;297-318/Domain: transmembrane #status predicted <TM3>
F;429-447/Domain: transmembrane #status predicted <TM4>
F;148-162,212-213/Disulfide bonds: #status predicted
F;161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.6%; Score 875; DB 2; Length 457;
Best Local Similarity 74.8%; Pred. No. 9.9e-73;
Matches 157; Conservative 24; Mismatches 29; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVETAGLQLIQLINVDVNOIVTNNRLKQOW 60
21 SEDESRLINDLFKSYKNVVRPAFAKDKVTVVGLQLIQLINVDVNOIVTNNRLKQOW 80
QY 61 VDYNLKNPDDYGGVKKIHIPSEKIMRPDLVLYNNADGFAIVKFTKVLQYTGHTWTP 120
DB 81 EDVHLKWDPEYGGIKKVRIPSSDIWRPDIIVLYNNADGFAIVQETKVLDDYTGKIIWLP 140
QY 121 PAIFKSCYEIIIVTHFPDEQNCMKLGTWYDGSVAINPESDQDLSNFMESGEWIK 180
DB 141 PAIFKSCYCEIMVTYFPDQLQNCMKLGTWYDGLVYINPDRDLSNFMESGEWYMKD 200
QY 181 SRGKHSVTVYSCCPDTPYLDITYHFVMQRL 210
DB 201 YRCWKHWVYDCPETPYLDITYHFLLQRL 230

RESULT 12

A24572
nicotinic acetylcholine receptor alpha-3 chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 08-Nov-1996
C;Accession: A24572
R;Boulter, J.; Evans, K.; Goldman, D.; Martin, G.; Treco, D.; Heinemann, S.; Patrick, J.
Nature 319, 368-374, 1986
A;Title: Isolation of a cDNA clone coding for a possible neuronal nicotinic acetylcholine
A;Reference number: A24572; MUID:86118671; PMID:3753746
A;Accession: A24572
A;Molecule type: mRNA
A;Residues: 1-499 <BOU>
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-499/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT>

Query Match 52.0%; Score 594.5; DB 2; Length 499;
Best Local Similarity 51.4%; Pred. No. 7.7e-47;
Matches 108; Conservative 39; Mismatches 62; Indels 1; Gaps 1;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVETAGLQLIQLINVDVNOIVTNNRLKQOW 60
DB 26 SEAEHRLFQVLFEDYNEIIRPVANVSHPVITQFVSMVSQLVKVDEVNQIMETNLWLKQIW 85
QY 61 VDYNLKNPDDYGGVKKIHIPSEKIMRPDLVLYNNADGFAIVKFTKVLQYTGHTWTP 120
DB 86 NDYKLNKPPSDYQGVFPMRPAEKIMRPDIIVLYNNADGFAIVQETKVLDDYTGKIIWLP 145
QY 121 PAIFKSCYEIIIVTHFPDEQNCMKLGTWYDGSVAINPESDQDLSNFMESGEWIK 180
DB 146 PAIFKSCCKIDVTYFPDYNQCTMKFGWSYDKAKIDLVLIGSSMNLKDYWESGEWAIK 205
QY 181 SRGKHSVTVYSCCPDTPYLDITYHFVMQRL 210
DB 206 APGYKHEIKYNCCEEI-YQDITYSLYIRRL 234

RESULT 13

A53956
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C;Accession: A53956; S21338
R;Mihovilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuro
A;Reference number: A53956; MUID:91114756; PMID:1989896
A;Accession: A53956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <MIH>
A;Cross-references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
submitted to the EMBL Data Library, June 1990
A;Description: Nucleotide sequence of the mature human nicotinic acetylcholine receptor
A;Reference number: S21338
A;Accession: S21338
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 30-503 <ANA>
A;Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C;Genetics:
A;Gene: GDB:CHRNA3
A;Cross-references: GDB:125219; OMIM:118503
A;Map position: 15q24-15q24
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match 52.0%; Score 594.5; DB 2; Length 503;
Best Local Similarity 51.0%; Pred. No. 7.7e-47;
Matches 107; Conservative 41; Mismatches 61; Indels 1; Gaps 1;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHROVETAGLQLIQLINVDVNOIVTNNRLKQOW 60
DB 30 SEAEHRLFQVLFEDYNEIIRPVANVSDPVIIHFVSMVSQLVKVDEVNQIMETNLWLKQIW 89
QY 61 VDYNLKNPDDYGGVKKIHIPSEKIMRPDLVLYNNADGFAIVKFTKVLQYTGHTWTP 120
DB 90 NDYKLNKPPSDYQGVFPMRPAEKIMRPDIIVLYNNADGFAIVQETKVLDDYTGKIIWLP 149
QY 121 PAIFKSCYEIIIVTHFPDEQNCMKLGTWYDGSVAINPESDQDLSNFMESGEWIK 180
DB 150 PAIFKSCCKIDVTYFPDYNQCTMKFGWSYDKAKIDLVLIGSSMNLKDYWESGEWAIK 209
QY 181 SRGKHSVTVYSCCPDTPYLDITYHFVMQRL 210
DB 210 APGYKHEIKYNCCEEI-YPDITYSLYIRRL 238

RESULT 14

S60589
acetylcholine receptor alpha chain precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C;Accession: S60589
R;Criado, M.; Alamo, L.; Navarro, A.
Neurochem. Res. 17, 281-287, 1992
A;Title: Primary structure of an agonist binding subunit of the nicotinic acetylcholi
A;Reference number: S60589; MUID:92319195; PMID:1620271
A;Accession: S60589
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-495 <CRI>
A;Cross-references: EMBL:X57032; NID:g297762; PIDN:CAA40348.1; PID:g297763
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-495/Product: acetylcholine receptor alpha chain #status predicted <MAT>

Query Match 51.5%; Score 588.5; DB 2; Length 495;

Best Local Similarity 50.5%; Pred. No. 2.7e-46;
Matches 106; Conservative 41; Mismatches 62; Indels 1; Gaps 1;

Qy 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLQLINVDVNOIVTNNRLKQOW 60
Db 22 SDAEHLRFLERLFEDYNEIIRPVANVSDPVITQFEVMSQLVKVDVNOIMETNLWLKQIW 81

Qy 61 VDYNLKWNPDYGGVKKTHIPSEKIWRPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 120
Db 82 NDYKLKWNPSDYDGAEFMRVPAEKIKWPDVLYNNAVGDFQVDDKTKALLKTYTGEVTWIP 141

Qy 121 PAIFKSYCEIIVTHPPFDEQNCMKLGTWTYDGSVVAINPESDQDPLSNFMSGEWVIKE 180
Db 142 PAIFKSSCKIDVTYFPDYQNCMTKFGWSYDKAKIDVLIGSSMNLADYWESEWAIK 201

Qy 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
Db 202 APGYKHKIKYNCCEI-YPDITYSLYIRRL 230

SULT 15
7040

nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal (version 2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C:Accession: A37040; S24595
R:Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
Neurosci. Lett. 111, 351-356, 1990
A:Title: Molecular cloning of human neuronal nicotinic receptor alpha-3-subunit.
A:Reference number: A37040; MUID:90245296; PMID:2336208
A:Accession: A37040
A:Molecule type: mRNA
A:Residues: 1-502 <FOR>
A:Cross-references: EMBL:X52239; NID:g177897; PIDN:AAC84176.1; PID:g177898
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor; transmembrane protein
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <MAT>

Query Match 51.5%; Score 588.5; DB 2; Length 502;
Best Local Similarity 50.5%; Pred. No. 2.8e-46;
Matches 106; Conservative 40; Mismatches 63; Indels 1; Gaps 1;

Qy 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLQLINVDVNOIVTNNRLKQOW 60
Db 29 SEAEHLRFLERLFEDYNEIIRPVANVSDPVITQFEVMSQLVKVDVNOIMETNLWLKQIW 88

Qy 61 VDYNLKWNPDYGGVKKTHIPSEKIWRPDLVLYNNADGDFAIKFTKVLLOYTGHITWTP 120
Db 89 NDYKLKWNPSDYDGAEFMRVPAEKIKWPDVLYNNAVGDFQVDDKTKALLKTYTGEVTWIP 148

Qy 121 PAIFKSYCEIIVTHPPFDEQNCMKLGTWTYDGSVVAINPESDQDPLSNFMSGEWVIKE 180
Db 149 PAIFKSSCKIDVTYFPDYQNCMTKFGWSYDKAKIDVLIGSSMNLADYWESEWAIK 208

Qy 181 SRGKHSVTYSCCPDTPYLDITYHFVMQRL 210
Db 209 APGYKHKIKYNCCEI-YPDITYSLYIRRL 237

Search completed: January 14, 2003, 16:58:18
Job time : 50 secs

Result No.	Score	Query %			DB	ID	Description
		Match	Length				
1	1116.5	97.7	482	1	ACHA_HUMAN	P02708 homo sapien	
2	1096	95.9	457	1	ACHA_BOVIN	P02709 bos taurus	
3	1096	95.9	457	1	ACHA_MOUSE	P04756 mus musculus	
4	1095	95.8	457	1	ACHA_RAT	P25108 rattus norv	
5	983	86.0	456	1	ACHA_CHICK	P09479 gallus gall	
6	915	80.1	461	1	ACHA_TORCA	P02711 torpedo cal	
7	910	79.6	461	1	ACHA_TORCA	P02710 torpedo cal	
8	888	77.7	457	1	ACH2_XENLA	P05377 xenopus lae	
9	882	77.2	456	1	ACHA_BRARE	P08880 brachydantio	
10	875	76.6	457	1	ACH1_XENLA	P22456 xenopus lae	
11	594.5	52.0	499	1	ACH3_RAT	P04757 rattus norv	
12	594.5	52.0	503	1	ACH3_HUMAN	P32297 homo sapien	
13	588.5	51.5	495	1	ACH3_BOVIN	Q07263 bos taurus	
14	583.5	51.0	496	1	ACH3_CHICK	P09481 gallus gall	
15	580.5	50.8	630	1	ACH4_RAT	P09483 rattus norv	
16	577.5	50.5	627	1	ACHA_HUMAN	P30581 homo sapien	
17	576	50.4	468	1	ACH5_HUMAN	P30532 homo sapien	
18	575.5	50.3	529	1	ACH2_HUMAN	Q15822 homo sapien	
19	571.5	50.0	512	1	ACH3_CARAU	P18845 carassius a	
20	571.5	50.0	622	1	ACH4_CHICK	P09482 gallus gall	
21	569.5	49.8	494	1	ACH6_HUMAN	Q15825 homo sapien	
22	564.5	49.4	511	1	ACH2_RAT	P12389 rattus norv	
23	564	49.3	452	1	ACH5_RAT	P20420 rattus norv	
24	562.5	49.2	528	1	ACH2_CHICK	P09480 gallus gall	
25	560.5	49.0	494	1	ACH6_CHICK	P49581 gallus gall	
26	553.5	48.4	462	1	ACHO_CARAU	P13908 carassius a	
27	553.5	48.4	493	1	ACH6_RAT	P43143 rattus norv	
28	552	48.3	567	1	ACH1_DROME	P09478 drosophila	
29	537	47.0	454	1	ACH5_CHICK	P26152 gallus gall	
30	536.5	46.9	458	1	ACHO_HUMAN	Q05901 homo sapien	
31	532.5	46.6	455	1	ACHO_CHICK	P43679 gallus gall	
32	532.5	46.6	464	1	ACHO_RAT	P12391 rattus norv	
33	532	46.5	516	1	ACH1_MANSE	P91766 manduca sex	

RA Talib S., Okarma T.B., Lebkowski J.S.;
 RT Differential expression of human nicotinic acetylcholine receptor
 RL alpha subunit variants in muscle and non-muscle tissues.";
 RN Nucleic Acids Res. 21:233-237(1993).
 RP [7]
 RP VARIANT SCMS SER-198.
 RX MEDLINE=95344777; PubMed=7619526;
 RA Sine S.M., Ohno K., Bouzat C., Auerbach A., Milone M., Pruitt J.N. II,
 RA Engel A.G.;
 RA "Mutation of the acetylcholine receptor alpha subunit causes a slow-
 RT channel myasthenic syndrome by enhancing agonist binding affinity.";
 RL Neuron 15:229-239(1995).
 RN [8]
 RP VARIANT SCMS LYS-262.
 RX MEDLINE=97026281; PubMed=8872460;
 RA Engel A.G., Ohno K., Milone M., Wang H.-L., Nakano S., Bouzat C.,
 RA Pruitt J.N. II, Hutchinson D.O., Bregman J.M., Bren N., Sieb J.P.,
 RA Sine S.M.;
 RA "New mutations in acetylcholine receptor subunit genes reveal
 RT heterogeneity in the slow-channel congenital myasthenic syndrome.";
 RL Hum. Mol. Genet. 5:1217-1227(1996).
 RN [9]
 RX VARIANTS SCMS SER-198; MET-201; ILE-299 AND ILE-314.
 RA MEDLINE=97301773; PubMed=9158151;
 RA Croxen R., Newland C., Beeson D., Oosterhuis H., Chauplannaz G.,
 RA Vincent A., Newsom-Davis J.;
 RA "Mutations in different functional domains of the human muscle
 RT acetylcholine receptor alpha subunit in patients with the
 RL slow-channel congenital myasthenic syndrome.";
 RL Hum. Mol. Genet. 6:767-774(1997).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
 CC MUSCLE) CHAINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 AND 2 (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS DIFFERENTIALLY EXPRESSED ONLY IN
 CC THE SKELETAL MUSCLE, WHEREAS ISOFORM 2 IS CONSTITUTIVELY EXPRESSED
 CC IN THE SKELETAL MUSCLE, BRAIN, HEART, KIDNEY, LIVER LUNG AND THYMUS.
 CC -1- DISEASE: THE ALPHA SUBUNIT IS THE MAIN FOCUS FOR ANTIBODY BINDING
 CC IN MYASTHENIA GRAVIS. MYASTHENIA GRAVIS IS CHARACTERIZED BY
 CC SPORADIC MUSCULAR FATIGABILITY AND WEAKNESS, OCCURRING CHIEFLY IN
 CC MUSCLES INNERVATED BY CRANIAL NERVES, AND CHARACTERISTICALLY
 CC IMPROVED BY CHOLINESTERASE-INHIBITING DRUGS.
 CC -1- DISEASE: DEFECTS IN CHRNA1 ARE ONE OF THE CAUSES OF THE SLOW-
 CC CHANNEL CONGENITAL MYASTHENIC SYNDROME (SCMS).
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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 CC or send an email to license@isb-sib.ch).

 DR EMBL; Y00762; CAA68731.1; -;
 DR EMBL; X17104; CAA34960.1; -;
 DR EMBL; X02502; CAA26344.1; -;
 DR EMBL; X02503; CAA26344.1; JOINED.
 DR EMBL; X02504; CAA26344.1; JOINED.
 DR EMBL; X02505; CAA26344.1; JOINED.
 DR EMBL; X02506; CAA26344.1; JOINED.
 DR EMBL; X02507; CAA26344.1; JOINED.
 DR EMBL; X02508; CAA26344.1; JOINED.
 DR EMBL; S77094; AAD14247.1; -;
 DR EMBL; X70108; CAA49705.1; ALT_SEQ.
 DR PIR; A03168; ACHUA1.
 DR PIR; S10148; S10148.

DR Genew; HGNC:1955; CHRNA1.
 DR MIN; 100690; -;
 DR MIN; 254210; -;
 DR MIN; 601462; -;
 DR InterPro; IPR000188; GABAA_receptor.
 DR InterPro; IPR001175; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Alternative splicing; transmembrane; Disease mutation.
 FT SIGNAL 1 20
 FT CHAIN 21 482
 FT DOMAIN 21 255
 FT TRANSMEM 256 280
 FT TRANSMEM 288 306
 FT TRANSMEM 322 341
 FT DOMAIN 342 453
 FT TRANSMEM 454 472
 FT DISULFID 173 187
 FT DISULFID 237 238
 FT CARBOHYD 186 186
 FT VARSPLIC 79 103
 FT VARIANT 198 198
 FT VARIANT 201 201
 FT VARIANT 262 262
 FT VARIANT 299 299
 FT VARIANT 314 314
 FT CONFLICT 415 415
 FT SEQUENCE 482 AA; 54545 MW; 8B307AD69B91A28B CRC64;
 SO
 Query Match 97.7%; Score 1116.5; DB 1; Length 482;
 Best Local Similarity 88.9%; Pred. No. 3.5e-94;
 Matches 209; Conservative 0; Mismatches 1; Indels 25; Gaps 1;
 Oy 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLQLINVDVNOIVTTNVLKQ-- 58
 Db 21 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLQLINVDVNOIVTTNVLKQGD 80
 Oy 59 -----QWVDYNLKNPDDYGVKKIHIPSEKIWRPDLVLYNN 95
 Db 81 MVDLPSPSCVTGLGVPLFSLHQLNEQWVDYNLKNPDDYGVKKIHIPSEKIWRPDLVLYNN 140
 Oy 96 ADGDFAIYKFTKVLQYTGHTTTPPAIFKSYCEIIVTHFFDEQNCMSKLGTTWYDGSV 155
 Db 141 ADGDFAIYKFTKVLQYTGHTTTPPAIFKSYCEIIVTHFFDEQNCMSKLGTTWYDGSV 200
 Oy 156 VAINPESQDPDLSNFMESGEWIKESRGWKHSVTVSCCPDTPYLDITVHFVQRL 210
 Db 201 VAINPESQDPDLSNFMESGEWIKESRGWKHSVTVSCCPDTPYLDITVHFVQRL 255
 RESULT 2
 ACHA_BOVIN
 ID ACHA_BOVIN STANDARD; PRT; 457 AA.
 AC P02709;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha chain precursor.
 GN CHRNA1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.

FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION.
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CONFLICT 13 13 C -> S (IN REF. 2 AND 3).
 SQ SEQUENCE 457 AA; 51938 MW; 5CB606D144F29436 CRC64;

Query Match 95.9%; Score 1096; DB 1; Length 457;
 Best Local Similarity 94.8%; Pred. No. 2.4e-92;
 Matches 199; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQIQLINVDENVQIVTNNVRLKQOW 60
 Db 21 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQIQLINVDENVQIVTNNVRLKQOW 80

QY 61 VDYNLKWNPDYGGVKKIHPSEKIWRPDLVLYNNADGFAIVKFKVLLQYTGHTWTP 120
 Db 81 VDYNLKWNPDYGGVKKIHPSEKIWRPDLVLYNNADGFAIVKFKVLLQYTGHTWTP 140

QY 121 PAIFKSYCEIIVTHFPDQNCMKLGTWYDGSVVAIINPESDQDPLSNFMSGEWVKE 180
 Db 141 PAIFKSYCEIIVTHFPDQNCMKLGTWYDGSVVAIINPESDQDPLSNFMSGEWVKE 200

181 SRGWKHSVTYSCPTPYLDITYHFVQMRL 210
 Db 201 ARGWKHWVFYSCPTPYLDITYHFVQMRL 230

RESULT 4
 ACHA_RAT
 ID ACHA_RAT STANDARD; PRT; 457 AA.
 AC P25108;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha chain precursor.
 GN CHRNA1 OR ACRA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=91099317; PubMed=1702709;
 RA Wittemann V., Stein E., Barg B., Konno T., Koenen M., Kues W.,
 RA Criado M., Hofmann M., Sakmann B.;
 RT "Primary structure and functional expression of the alpha-, beta-,
 RT gamma-, delta- and epsilon-subunits of the acetylcholine receptor
 RT from rat muscle".
 RT Eur. J. Biochem. 194:437-448(1990).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
 CC MUSCLE) CHAINS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 CC EMBL; X74832; CAA52826.1; .
 CC PIR; S13872; S13872.
 CC InterPro; IPR000188; GABAA_receptor.
 CC InterPro; IPR001175; Neur_chan.
 CC Pfam; PF02931; Neur_chan_LBD; 1.
 CC Pfam; PF02932; Neur_chan_memb; 1.

DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane.
 FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 457 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
 FT CHAIN. CHAIN.
 FT DOMAIN 21 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 255 POTENTIAL.
 FT TRANSMEM 263 281 POTENTIAL.
 FT TRANSMEM 297 316 POTENTIAL.
 FT DOMAIN 317 428 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 429 447 POTENTIAL.
 FT DISULFID 148 162 BY SIMILARITY.
 FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 457 AA; 51866 MW; 776AE3B8DF68F3 CRC64;

Query Match 95.8%; Score 1095; DB 1; Length 457;
 Best Local Similarity 94.8%; Pred. No. 3e-92;
 Matches 199; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQIQLINVDENVQIVTNNVRLKQOW 60
 Db 21 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQIQLINVDENVQIVTNNVRLKQOW 80

QY 61 VDYNLKWNPDYGGVKKIHPSEKIWRPDLVLYNNADGFAIVKFKVLLQYTGHTWTP 120
 Db 81 VDYNLKWNPDYGGVKKIHPSEKIWRPDLVLYNNADGFAIVKFKVLLQYTGHTWTP 140

QY 121 PAIFKSYCEIIVTHFPDQNCMKLGTWYDGSVVAIINPESDQDPLSNFMSGEWVKE 180
 Db 141 PAIFKSYCEIIVTHFPDQNCMKLGTWYDGSVVAIINPESDQDPLSNFMSGEWVKE 200

QY 181 SRGWKHSVTYSCPTPYLDITYHFVQMRL 210
 Db 201 ARGWKHWVFYSCPTPYLDITYHFVQMRL 230

RESULT 5
 ACHA_CHICK
 ID ACHA_CHICK STANDARD; PRT; 456 AA.
 AC P09479;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha chain precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88283624; PubMed=3267226;
 RA Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.;
 RT "Genes expressed in the brain define three distinct neuronal
 RT nicotinic acetylcholine receptors.";
 RL EMBO J. 7:595-601(1988).
 RN [2]
 RP SEQUENCE OF 1-12 FROM N.A.
 RX MEDLINE=8714271; PubMed=3821734;
 RA Klarsfeld A., Daubas P., Bourachot B., Changeux J.-P.;
 RT "A 5'-flanking region of the chicken acetylcholine receptor alpha-
 RT subunit gene confers tissue specificity and developmental control of
 RT expression in transfected cells.";
 RL Mol. Cell. Biol. 7:951-955(1987).
 RN [3]
 RP SEQUENCE OF 180-227 AND 260-333 FROM N.A.
 RX MEDLINE=84206570; PubMed=6327170;

RA Ballivet M., Nef P., Stalder R., Fulpius B.;
 RT "Genomic sequences encoding the alpha-subunit of acetylcholine
 RL receptor are conserved in evolution.";
 RN Cold Spring Harb. Symp. Quant. Biol. 48:83-87(1983).
 RN [4]
 RN SEQUENCE OF 21-44.
 RX MEDLINE=85270494; PubMed=3860855;
 RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
 RA Ray N., Raftery M.A.;
 RT "Brain and muscle nicotinic acetylcholine receptors are different but
 RT homologous proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 CC DELTA, AND GAMMA CHAINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 DR EMBL; X07330; CAA30282.1; JOINED.
 DR EMBL; X07331; CAA30282.1; JOINED.
 DR EMBL; X12434; CAA30282.1; JOINED.
 DR EMBL; X12435; CAA30282.1; JOINED.
 DR EMBL; X12436; CAA30282.1; JOINED.
 DR EMBL; X07335; CAA30282.1; JOINED.
 DR EMBL; AJ250359; CAB59624.1; -.
 DR EMBL; AF051909; AACU6012.1; -.
 DR EMBL; M14808; AAA48565.1; -.
 DR EMBL; M14809; AAA48564.1; -.
 DR PIR; S00376; ACCHAN.
 DR PIR; A25738; A25738.
 DR InterPro; IPRO00188; GABAA_receptor.
 DR InterPro; IPRO01175; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 DR Transmembrane.
 FT SIGNAL 1 20
 FT CHAIN 21 456
 FT
 FT ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
 FT CHAIN.
 FT EXTRACELLULAR.
 FT
 FT DOMAIN 21 229
 FT TRANSMEM 230 254
 FT TRANSMEM 262 280
 FT TRANSMEM 296 315
 FT DOMAIN 316 427
 FT TRANSMEM 428 446
 FT TRANSMEM 447 161
 FT DISULFID 141 161
 FT DISULFID 211 212
 FT CARBOHYD 160 160
 FT CONFLICT 33 33
 FT CONFLICT 33 33
 SQ SEQUENCE 456 AA; 52183 MW; 0B31B6EABD7B4DA2 CRC64;

Query Match 86.08; Score 983; DB 1; Length 456;
 Best Local Similarity 84.28; Pred. No. 4.7e-82;
 Matches 176; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

OY 2 EHETRLVAKLPKDYSSVVRPVEDHQVVEVTAGLIQLIQLINVDENVQIVTNNRKLKQOW 61
 DB 21 EHETRLVDDLPREYSKVVRPVENRDVAVVTGVLQIQLINVDENVQIVTNNRKLKQOW 80

OY 62 DYNLKNPDDYGGVKIHPSEKIWRPDLVLYNNADGFAIVKFKVLLQVLTGHTWTPP 121
 DB 81 DYNLKNPDDYGGVKIHPSEKIWRPDLVLYNNADGFAIVKFKVLLQVLTGHTWTPP 140
 OY 122 AIFKSYCEIIVTHFPDFQNCMSKLGWTYDGSVVAINPESDQDLSNFMESGEWIKES 181
 DB 141 AIFKSYCEIIVTHFPDFQNCMSKLGWTYDGSVVAINPESDQDLSNFMESGEWIKES 200
 OY 182 RGWHSVSYSCCPOTPYLDITYHFVQRL 210
 DB 201 RGWHSVSYSCCPOTPYLDITYHFVQRL 229
 RESULT 6
 ACHA_TORMA STANDARD; PRT; 461 AA.
 ID PO2711;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor protein, alpha chain precursor.
 OS Torpedo marmorata (Marbled electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squalia; Hypnosqualea; Pristiogaster; Batoidae;
 OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
 OX NCBI_TaxID=7788;
 RN [1]
 RP SEQUENCE OF 1-335 AND 341-411 FROM N.A.
 RX MEDLINE=83064520; PubMed=6183641;
 RA Sumikawa K., Houghton M., Smith J.C., Bell L., Richards B.M.,
 RA Barnard E.A.;
 RT "The molecular cloning and characterisation of cDNA coding for the
 RT alpha subunit of the acetylcholine receptor.";
 RL Nucleic Acids Res. 10:5809-5822(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83169822; PubMed=6572962;
 RA Devillers-Thiery A., Giraudat J., Bentabollet M., Changeux J.-P.;
 RT "Complete mRNA coding sequence of the acetylcholine binding alpha-
 RT subunit of Torpedo marmorata acetylcholine receptor: a model for the
 RT transmembrane organization of the polypeptide chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2067-2071(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85171452; PubMed=6549423;
 RA Devillers-Thiery A., Giraudat J., Bentabollet M., Klarsfeld A.,
 RA Changeux J.-P.;
 RT "Molecular genetics of Torpedo marmorata acetylcholine receptor.";
 RL Adv. Exp. Med. Biol. 181:17-29(1984).
 RN [4]
 RP SEQUENCE OF 1-79 FROM N.A.
 RX MEDLINE=84206529; PubMed=6327147;
 RA Barnard E.A., Beeson D., Bilbe G., Brown D.A., Constanti A.,
 RA Conti-Tronconi B.M., Dolly J.O., Dunn S.M.J., Mehraban F.,
 RA Richards B.M., Smart T.G.;
 RT "Acetylcholine and GABA receptors: subunits of central and peripheral
 RT receptors and their encoding nucleic acids.";
 RL Cold Spring Harb. Symp. Quant. Biol. 48:109-124(1983).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 CC DELTA, AND GAMMA CHAINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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FT	263	281
TRANSMEM	297	316
TRANSMEM	317	428
DOMAIN	429	447
TRANSMEM	148	162
DISULFID	212	213
DISULFID	161	161
FT	457	52107
FT	457	AA;
FT		202A84A150C4DB11
FT		CRC64;
FT		ASSOCIATED WITH RECEPTOR ACTIVATION.
FT		N-LINKED (GLCNAC..?) (PROBABLE).
FT		CYTOPLASMIC.

Query Match 77.7%; Score 888; DB 1; Length 457;
Best Local Similarity 75.2%; Pred. No. 2.1e-73;
Matches 158; Conservative 23; Mismatches 29; Indels 0; Gaps 0;

1	QY	SEHETRLVAKLKFDDKSSVVRPVEDHHRQVYEVTAGLQIOLINVDENVQIVTNTNRLKQOM	60
21	Db	TDHETRLIGDLGFANFKVVRPVEYTKDQVVVTVGQLQIOLINVDENVQIVSTNIRLKQOM	80
61	QY	VDYNLKNPDDGKGVKKIHPSEKTRPDLVLYNNADGDFATVKFTKVLQYTGHTWTP	120
81	Db	RDVNLKWDPAKGGVKKIIRIPSDVWSPDLVLYNNADGDFALSKDTKILLETGKITWTP	140
121	QY	PAIFKSYCEIIVTFEPDQNGSMKLGTTWYDGSVVAINPESDQDPDLSNFMESGEWVKE	180
141	Db	PAIFKSYCEIIVTFEPDQNGSMKFGTWYDGSLLVINPERDRDPLSNFMASGEWMMKD	200
181	QY	SRGWKHUSVYSCCPDPPIYDITVHFVNRQL	210
201	Db	YRCWKHWYITCTCPDKPIYDITVHFVLRQL	230

RESULT 9				
ID	ACHA_BRARE	ACHA_BRARE	STANDARD;	PRT;
AC	Q98880;			456 AA.
DT	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Acetylcholine receptor protein, alpha chain precursor.			
GN	CHRNA1 OR NIC1.			
OS	Brachydanio rerio (zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			

RX MEDLINE=96133893; PubMed=9475746;
 RA Sepich D.S., Wegner J.J., O'Shea S., Westerfield M.:
 RT "An altered intron inhibits synthesis of the acetylcholine receptor
 RL alpha-subunit in the paralyzed zebrafish mutant ncl1".
 RL Genetics 148:361-372(1998).
 CC -I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.

-|- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC
CC
CC
CC
SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC
-|- DETECTION METHOD: By immunoblotting.
CC
CC
-|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY .
CC
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CC
CC EMBL; U70436; AAB09701.1; -
CC
CC EMBL; U70437; AAB09770.1; -
CC
CC EMBL; U70438; AAB16917.1; -
CC
CC ZFIN; ZDB-GENE-980526-137; chrnal.
CC
CC InterPro: IPR000188; GARAAX chnrcal.

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DR InterPro: IPR001175; Neur_chan_1.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_LBD; 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR TIGRFAMs: TIGR00860; LIC; 1.
DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 456
BY SIMILARITY.
ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
CHAIN.
FT DOMAIN 21 230
FT TRANSMEM 231 255
FT TRANSMEM 263 281
FT TRANSMEM 297 316
FT TRANSMEM 317 428
FT TRANSMEM 429 447
FT DISULFID 148 162
FT DISULFID 212 213
BY SIMILARITY.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION
(BY SIMILARITY).
N-LINKED (GLCNAC... ) (POTENTIAL).
CARBOHYD 161
SEQUENCE 456 AA; 52100 MW; 336825C5E358G6F3 CRC64;
Query Match 77.2%; Score 882; DB 1; Length 456;
Best Local Similarity 75.7%; Pred. No. 7.3e-73;
Matches 159; Conservative 22; Mismatches 29; Indels 0; Gaps 0;
QY 1 SEHETRLVAKLFKDYSSVVRPVVEDHQVVEVTAGLIQLIQLINVDVNVQIVTNNVRLKQOW 60
DB 21 SEDETRLVKTLFTGYKNKVRPVSHFDPVVTGVLQIQLISVDVNVQIVTNNVRLKQOW 80
QY 61 VDNLKNWPDYGGVKKIHPSEKIWRPDLVLYNNADGFAIVKFKVLLQVTHITWTP 120
DB 81 KDVHLQWNPDDYGGIRKIRIPSTDLKPKDLVLYNNADGFAIVKFKVLLQVTHITWTP 140
QY 121 PAIFKSYCEIIVTHFPFDEQNCMKLGTWYDGSVVAINPESDQDPLSNFMSGEWVKE 180
DB 141 PAIFKSYCEIIVTHFPFDEQNCMKLGTWYDGSVVAINPESDQDPLSNFMSGEWVMD 200
QY 181 SRGKHSVYSCCPDTPYLDITYHFVQRL 210
DB 201 YRSWKHWYVYACPDTPYLDITYHFVQRL 230
PRT; 457 AA.
RESULT 10
ACHL_XENLA
ID ACHL_XENLA STANDARD; PRT; 457 AA.
AC P22456;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-1A chain precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Muscle;
MEDLINE=90136925; Pubmed=2300185;
RA Hartman D.S.; Claudio T.;
RT "Coexpression of two distinct muscle acetylcholine receptor alpha-
subunits during development.";
RL Nature 343:372-375(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBRANE.
CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
MUSCLE) CHAINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

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CC -!- TISSUE SPECIFICITY: OOCYTES.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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EMBL: X17244; CAA35109.1; -
PIR: S08162; S08162.
InterPro: IPR001188; GABAA_receptor.
Pfam: PF02931; Neur_chan_LBD; 1.
Pfam: PF02932; Neur_chan_LBD; 1.
PRINTS: PR00252; NRIONCHANNEL.
TIGRFAMs: TIGR00860; LIC; 1.
PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 457
ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-1A
CHAIN.
EXTRACELLULAR.
CYTOPLASMIC.
ASSOCIATED WITH RECEPTOR ACTIVATION.
N-LINKED (GLCNAC... ) (PROBABLE).
SEQUENCE 457 AA; 52457 MW; 8728D227D905ED10 CRC64;
Query Match 76.6%; Score 875; DB 1; Length 457;
Best Local Similarity 74.8%; Pred. No. 3.2e-72;
Matches 157; Conservative 24; Mismatches 29; Indels 0; Gaps 0;
QY 1 SEHETRLVAKLFKDYSSVVRPVVEDHQVVEVTAGLIQLIQLINVDVNVQIVTNNVRLKQOW 60
DB 21 SEDETRLVKTLFTGYKNKVRPVSHFDPVVTGVLQIQLISVDVNVQIVTNNVRLKQOW 80
QY 61 VDNLKNWPDYGGVKKIHPSEKIWRPDLVLYNNADGFAIVKFKVLLQVTHITWTP 120
DB 81 EDVHLKWDPEYGGIKKVRIPSSDIWRPDLVLYNNADGFAIVKFKVLLQVTHITWTP 140
QY 121 PAIFKSYCEIIVTHFPFDEQNCMKLGTWYDGSVVAINPESDQDPLSNFMSGEWVKE 180
DB 141 PAIFKSYCEIIVTHFPFDEQNCMKLGTWYDGSVVAINPESDQDPLSNFMSGEWVMD 200
QY 181 SRGKHSVYSCCPDTPYLDITYHFVQRL 210
DB 201 YRSWKHWYVYACPDTPYLDITYHFVQRL 230
PRT; 499 AA.
RESULT 11
ACH3_RAT
ID ACH3_RAT STANDARD; PRT; 499 AA.
AC P04757;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neuroal acetylcholine receptor protein, alpha-3 chain precursor.
GN CHRNA3 OR ACRA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=86118671; Pubmed=3753746;

```

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OM protein - protein search, using sw model

Run on: January 14, 2003, 16:49:47 ; Search time 112 Seconds
(without alignments)
386.338 Million cell updates/sec

Title: US-09-820-339A-2
Perfect score: 1143
Sequence: 1 SEHETRLVAKLFKDYSSVVR.....SCDPTPYLDITYHFVQRL 210

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
tal number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1139	99.7	269	4 Q9BRE6	Q9bre6 homo sapien
2	1096	95.9	457	6 Q9XS62	Q9xs62 canis famil
3	594.5	52.0	341	11 Q8V111	Q8v111 mus musculu
4	594.5	52.0	489	4 Q9BR44	Q9br44 homo sapien
5	594.5	52.0	499	11 Q8VHH6	Q8vhh6 mus musculu
6	594.5	52.0	499	11 Q8R4G9	Q8r4g9 mus musculu
7	580.5	50.8	629	11 Q923N8	Q923n8 mus musculu
8	580.5	50.8	641	11 Q923N7	Q923n7 mus musculu
9	575.5	50.3	629	11 Q9ET51	Q9et51 mus musculu
10	571	50.0	475	6 Q8SPU7	Q8spu7 bos taurus
11	565.5	49.5	494	11 Q9R0W9	Q9r0w9 mus musculu
12	564	49.3	432	11 Q9QXK6	Q9qxk6 mus musculu
13	563.5	49.3	512	11 Q91X60	Q91x60 mus musculu
14	554	48.5	595	5 P91764	P91764 myzus persi
15	544	47.6	537	5 Q9U941	Q9u941 myzus persi
16	543	47.5	772	5 Q9W3G6	Q9w3g6 drosophila

17	543	47.5	776	5	O44202	O44202 drosophila
18	543	47.5	795	5	O18394	O18394 drosophila
19	541	47.3	531	5	O96632	O96632 heliothis v
20	538.5	47.1	464	11	Q8R5H3	Q8r5h3 mus musculu
21	538	47.1	515	5	O46133	O46133 locusta mig
22	536	46.9	540	5	O46134	O46134 locusta mig
23	532	46.5	523	5	O46128	O46128 heliothis v
24	531	46.5	533	5	Q8WRS1	Q8wrs1 chilo suppr
25	527	46.1	568	5	Q9NFR5	Q9nfr5 drosophila
26	524	45.8	532	5	Q9U940	Q9u940 myzus persi
27	521	45.6	494	5	Q8T7S3	Q8t7s3 drosophila
28	520.5	45.5	580	5	Q9VC72	Q9vc72 drosophila
29	518	45.3	523	5	Q8T7R9	Q8t7r9 drosophila
30	516.5	45.2	502	5	Q9N5B7	Q9n5b7 caenorhabdi
31	514.5	45.0	573	5	Q9GQU9	Q9gqu9 caenorhabdi
32	513	44.9	559	5	O46132	O46132 locusta mig
33	512	44.8	494	5	Q8T7S1	Q8t7s1 drosophila
34	510	44.6	552	5	P91765	P91765 myzus persi
35	509	44.5	494	5	Q8T7S2	Q8t7s2 drosophila
36	503.5	44.1	545	5	O96631	O96631 heliothis v
37	499	43.7	501	5	Q9XZ14	Q9xz14 heliothis v
38	498.5	43.6	484	13	Q9PTS8	Q9pts8 gallus gall
39	498.5	43.6	509	5	Q8T7S0	Q8t7s0 drosophila
40	498	43.6	807	5	Q8T7V5	Q8t7v5 drosophila
41	496.5	43.4	552	5	Q9VC74	Q9vc74 drosophila
42	492	43.0	311	5	Q9VW18	Q9vw18 drosophila
43	491	43.0	496	5	Q9XZ13	Q9xz13 heliothis v
44	490	42.9	238	5	Q8SXP7	Q8sxp7 drosophila
45	486	42.5	536	5	Q8T0Y9	Q8t0y9 aplysia cal

ALIGNMENTS

RESULT 1

Q9BRE6 ID Q9BRE6 PRELIMINARY; PRT; 269 AA.

AC Q9BRE6; 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Similar to cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MUSCLE;

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.

DR EMBL; BC006314; AAR06314.1; -

DR InterPro; IPR000188; GABAA_receptor.

DR InterPro; IPR001175; Neur_channel.

DR Pfam; PF02931; Neur_chan_LBD; 1.

DR Pfam; PF02932; Neur_chan_memb; 1.

DR PRINTS; PR00252; NRIONCHANNEL.

DR PROSITE; PS00236; NEURONTR_ION_CHANNEL; 1.

KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Transmembrane.

SQ SEQUENCE 269 AA; 30769 MW; 1874BFB614CEF18F CRC64;

Query Match 99.7%; Score 1139; DB 4; Length 269;
Best local Similarity 99.5%; Pred. No. 1.4e-96;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Caps 0;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHQRVVEVTAGLQLIQLINDEVNQIVTTNRLKQOW 60

DB 21 SEHETRLVAKLFKDYSSVVRPVEDHQRVVEVTAGLQLIQLINDEVNQIVTTNRLKQOW 80

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QY 61 VDYNLKNWPDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
DB 81 VDYNLKNWPDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 140
QY 121 PAIFKSYCEIIVTHPPFQNCMSKLGWTYDGSVVAINPESDQDPLSNFMSGGEWVKE 180
DB 141 PAIFKSYCEIIVTHPPFQNCMSKLGWTYDGSVVAINPESDQDPLSNFMSGGEWVKE 200
QY 181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
DB 201 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 230

RESULT 2
Q9XS62
ID Q9XS62 PRELIMINARY; PRT; 457 AA.
AC Q9XS62;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB 121 PAIFKSYCEIIVTHPPFQNCMSKLGWTYDGSVVAINPESDQDPLSNFMSGGEWVKE 180
DB 141 PAIFKSYCEIIVTHPPFQNCMSKLGWTYDGSVVAINPESDQDPLSNFMSGGEWVKE 200
QY 181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
DB 201 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 230

RESULT 3
Q8V111
ID Q8V111 PRELIMINARY; PRT; 341 AA.
AC Q8V111;
DT 01-MAR-2002 (TREMBLrel. 20, Created)

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DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 3 subunit (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kuo Y.-P., Lukas R.J.;
RT 'Expression of mouse nicotinic acetylcholine receptor genes in the
RT developing thymus.';
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF325346; AAL37362.1; -.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
KW Receptor.
FT NON_TER 341 341
SQ SEQUENCE 341 AA; 39386 MW; FB8325B5DB07E139 CRC64;

Query Match 52.0%; Score 594.5; DB 11; Length 341;
Best Local Similarity 51.4%; Pred. No. 1.7e-46;
Matches 108; Conservative 39; Mismatches 62; Indels 1; Gaps 1;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDENVQIVTNNVRLKQW 60
DB 26 SEAEHRLFOYLPEDYNEIIRPVANVSHPVIIQFEVSMQVQVDEVNQIMETNLKQIW 85
QY 61 VDYNLKNWPDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIKFTKVLQYTGHTWTP 120
DB 86 NDYKILKWPESDQYQGVFMRVPAEKIKWPKDVLVLYNNADGDFQVDDRTKALLKVTGEVTP 145
QY 121 PAIFKSYCEIIVTHPPFQNCMSKLGWTYDGSVVAINPESDQDPLSNFMSGGEWVKE 180
DB 146 PAIFKSSCKIDVTYFPDYQNCYCTMFGWSYDKAKIDLVLGSSMNLKDYWESGEWAIRK 205
QY 181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
DB 206 APGYAKHEIKYNCCEI-YQDITYSLYIRRL 234

RESULT 4
Q9BRR4
ID Q9BRR4 PRELIMINARY; PRT; 489 AA.
AC Q9BRR4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to cholinergic receptor, nicotinic, alpha polypeptide 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; BC006114; AA06114.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR000188; GABAA_receptor.
DR InterPro; IPR001175; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.

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DR TIGRFS: TIGR00860; LIC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 489 AA; 55636 MW; F8C4F79BDC30A44E CRC64;

Query Match 52.0%; Score 594.5; DB 4; Length 489;
Best Local Similarity 51.0%; Pred. No. 2.7e-46;
Matches 107; Conservative 41; Mismatches 61; Indels 1; Gaps 1;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHQRQVETAGLQIOLINDEVNQIVTNNRLKQW 60
DB 32 SEAEHRLVAKLFKDYSSVVRPVEDHQRQVETAGLQIOLINDEVNQIVTNNRLKQW 91
QY 61 VDYNLKKNPDYGGVKKIHPSEKIRPDLYNNADGFAIVKFTKVLQYTGHTWTP 120
DB 92 NDYKLKKNPSDYGGAEMFVRPAQKIWKPDVLYNNADGFAIVKFTKVLQYTGHTWTP 151
QY 121 PAIFKSYCEIIVTHFPFDEQNCMKLGTWTYDGSVVAINPESDQDLSNFMESGEWIK 180
DB 152 PAIFKSSCKIDVTYFPFDYQNTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIK 211
QY 181 SRGKHSVTVSCCPDTPYLDITYHFVMORL 210
DB 212 APGYKHEIKYNCCEI-YQDITYSLYIRRL 240

RESULT 5
Q8VHH6 PRELIMINARY; PRT; 499 AA.
AC Q8VHH6;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Neuronal nicotinic acetylcholine receptor alpha 3 subunit.
GN CHRNA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RA Brill J., Becker K., Becker C.-M.;
RT "Mouse neuronal nicotinic acetyl choline receptor alpha 3 subunit mRNA";
RW Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
SQ SEQUENCE 499 AA; 57125 MW; D21650F6A6D7C14B CRC64;

Query Match 52.0%; Score 594.5; DB 11; Length 499;
Best Local Similarity 51.4%; Pred. No. 2.8e-46;
Matches 108; Conservative 39; Mismatches 62; Indels 1; Gaps 1;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHQRQVETAGLQIOLINDEVNQIVTNNRLKQW 60
DB 26 SEAEHRLVAKLFKDYSSVVRPVEDHQRQVETAGLQIOLINDEVNQIVTNNRLKQW 85
QY 61 VDYNLKKNPDYGGVKKIHPSEKIRPDLYNNADGFAIVKFTKVLQYTGHTWTP 120
DB 86 NDYKLKKNPSDYGGAEMFVRPAQKIWKPDVLYNNADGFAIVKFTKVLQYTGHTWTP 145
QY 181 SRGKHSVTVSCCPDTPYLDITYHFVMORL 210
DB 212 APGYKHEIKYNCCEI-YQDITYSLYIRRL 240

RESULT 6
Q8R4G9 PRELIMINARY; PRT; 499 AA.
AC Q8R4G9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 3 subunit.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DEA/21BG; TISSUE=ADRENAL GLAND;
RA Lautner M.A., Stitzel J.A.;
RT "Cloning of mouse nicotinic acetylcholine receptor alpha 3 subunit cDNA";
RW Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF472588; AAL84757.1;
KW Receptor.
SQ SEQUENCE 499 AA; 57109 MW; 721650E3F38D00FD CRC64;

Query Match 52.0%; Score 594.5; DB 11; Length 499;
Best Local Similarity 51.4%; Pred. No. 2.8e-46;
Matches 108; Conservative 39; Mismatches 62; Indels 1; Gaps 1;

QY 1 SEHETRLVAKLFKDYSSVVRPVEDHQRQVETAGLQIOLINDEVNQIVTNNRLKQW 60
DB 26 SEAEHRLVAKLFKDYSSVVRPVEDHQRQVETAGLQIOLINDEVNQIVTNNRLKQW 85
QY 61 VDYNLKKNPDYGGVKKIHPSEKIRPDLYNNADGFAIVKFTKVLQYTGHTWTP 120
DB 86 NDYKLKKNPSDYGGAEMFVRPAQKIWKPDVLYNNADGFAIVKFTKVLQYTGHTWTP 145
QY 181 SRGKHSVTVSCCPDTPYLDITYHFVMORL 210
DB 206 APGYKHEIKYNCCEI-YQDITYSLYIRRL 234

RESULT 7
Q923N8 PRELIMINARY; PRT; 629 AA.
AC Q923N8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE B401117.2.1 (cholinergic receptor, nicotinic, alpha polypeptide 4 (isoform 1)).
GN CHRNA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Wall M.;
RW Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL450341; CAC40724.1;
DR InterPro; IPR000188; GABAA_receptor.

